

Match length 122
 % identity 87
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398082
 Seq. ID LIB3431-010-P1-K1-G8
 Method BLASTX
 NCBI GI g115796
 BLAST score 737
 E value 2.0e-78
 Match length 148
 % identity 96
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 398083
 Seq. ID LIB3431-010-P1-K1-G9
 Method BLASTX
 NCBI GI g2737973
 BLAST score 742
 E value 5.0e-79
 Match length 145
 % identity 96
 NCBI Description (U83625) protein kinase ZmMEK1 [Zea mays]

Seq. No. 398084
 Seq. ID LIB3431-010-P1-K1-H10
 Method BLASTX
 NCBI GI g3551523
 BLAST score 247
 E value 6.0e-21
 Match length 156
 % identity 37
 NCBI Description (AB017026) oxysterol-binding protein [Mus musculus]

Seq. No. 398085
 Seq. ID LIB3431-010-P1-K1-H11
 Method BLASTX
 NCBI GI g231610
 BLAST score 257
 E value 4.0e-22
 Match length 74
 % identity 76
 NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir_PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

09E34016 - 101000

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Seq. No.      398090
Seq. ID      LIB3431-010-P1-N1-A3
Method       BLASTN
NCBI GI      g218209
BLAST score   124
E value      3.0e-63
Match length  248
% identity    98
NCBI Description  Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
```

[illegible]

Seq. No.	398095
Seq. ID	LIB3431-010-P1-N1-B4
Method	BLASTN

0964015-101000

```
Seq. No.      398112
Seq. ID       LIB3431-010-P1-N1-E9
Method        BLASTN
NCBI GI       g20181
BLAST score    160
E value        1.0e-84
Match length   179
% identity     98
NCBI Description  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
```

```
Seq. No.          398113
Seq. ID           LIB3431-010-P1-N1-F1
Method            BLASTN
NCBI GI           g218207
BLAST score       217
E value           1.0e-119
Match length      221
% identity         100
NCBI Description   Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS1139
```

```
Seq. No.      398114
Seq. ID       LIB3431-010-P1-N1-F11
Method        BLASTN
NCBI GI       g6016845
BLAST score    204
E value       1.0e-111
Match length   240
% identity     96
NCBI Description  Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
```

```
Seq. No.      398115
Seq. ID      LIB3431-010-P1-N1-F12
Method       BLASTX
NCBI GI      g266893
BLAST score   637
E value      8.0e-67
Match length  123
% identity    98
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi_322416_pir_S28172_ribulose-bisphosphate carboxylase
                  activase - cucumber >gi_18284_emb_CAA47906 (X67674)
```

rubisco activase [Cucumis sativus]

Seq. No. 398116
 Seq. ID LIB3431-010-P1-N1-F3
 Method BLASTN
 NCBI GI g288058
 BLAST score 53
 E value 6.0e-21
 Match length 73
 % identity 93
 NCBI Description Z.mays S13 mRNA for cytoplasmic ribosomal protein S13

Seq. No. 398117
 Seq. ID LIB3431-010-P1-N1-G1
 Method BLASTN
 NCBI GI g2661765
 BLAST score 50
 E value 4.0e-19
 Match length 82
 % identity 90
 NCBI Description Zea mays mRNA for putative porphobilinogen deaminase

Seq. No. 398118
 Seq. ID LIB3431-010-P1-N1-G11
 Method BLASTN
 NCBI GI g218154
 BLAST score 80
 E value 6.0e-37
 Match length 145
 % identity 100
 NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No. 398119
 Seq. ID LIB3431-010-P1-N1-G12
 Method BLASTN
 NCBI GI g2662340
 BLAST score 269
 E value 1.0e-150
 Match length 316
 % identity 96
 NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 398120
 Seq. ID LIB3431-010-P1-N1-G2
 Method BLASTX
 NCBI GI g125606
 BLAST score 250
 E value 2.0e-21
 Match length 59
 % identity 86
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
 pyruvate kinase (EC 2.7.1.40) - potato
 >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
 tuberosum]

Seq. No. 398121

000001010000

Seq. ID LIB3431-010-P1-N1-G5
 Method BLASTX
 NCBI GI g548603
 BLAST score 225
 E value 2.0e-18
 Match length 56
 % identity 80
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
 barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 398122
 Seq. ID LIB3431-010-P1-N1-G7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 297
 E value 5.0e-27
 Match length 67
 % identity 85
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 398123
 Seq. ID LIB3431-010-P1-N1-G8
 Method BLASTX
 NCBI GI g132096
 BLAST score 154
 E value 3.0e-10
 Match length 29
 % identity 100
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
 (RUBISCO SMALL SUBUNIT A) >gi_68095_pir_RKRZS6
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_
 (D00644) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa]

Seq. No. 398124
 Seq. ID LIB3431-010-P1-N1-G9
 Method BLASTX
 NCBI GI g3126854
 BLAST score 300
 E value 2.0e-27
 Match length 57
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398125
 Seq. ID LIB3431-010-P1-N1-H1
 Method BLASTX
 NCBI GI g606817
 BLAST score 154
 E value 4.0e-10
 Match length 28
 % identity 100
 NCBI Description (U08404) carbonic anhydrase [Oryza sativa]
 >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic

056840163-303000

```
Seq. No.      398127
Seq. ID      LIB3431-010-P1-N1-H4
Method       BLASTX
NCBI GI      g548605
BLAST score   239
E value      1.0e-28
Match length  80
% identity    89
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                >gi_539055_pir_A48527 photosystem I protein psaK precursor
                - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                [Hordeum vulgare]
```

Seq. No.	398128
Seq. ID	LIB3431-010-P1-N1-H6
Method	BLASTN
NCBI GI	g1136121
BLAST score	321
E value	0.0e+00
Match length	324
% identity	100
NCBI Description	O.sativa mRNA for alpha-tubulin (clone OSTA-136)

```
Seq. No.      398129
Seq. ID      LIB3431-010-P1-N1-H7
Method       BLASTN
NCBI GI      g2737972
BLAST score   38
E value      6.0e-12
Match length  74
% identity   88
NCBI Description Zea mays protein kinase ZmMEK1 mRNA, complete cds
```

```
Seq. No.          398130
Seq. ID           LIB3431-011-P1-K1-A10
Method            BLASTX
NCBI GI           g1742187
BLAST score       170
E value           6.0e-12
Match length      121
% identity        35
NCBI Description   (D90771) ORF ID:o260#14; similar to [SwissProt Accession
                  Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_
                  (D90772) ORF ID:o260#14; similar to [SwissProt Accession
```


% identity 83
 NCBI Description (AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No. 398136
 Seq. ID LIB3431-011-P1-K1-B12
 Method BLASTX
 NCBI GI g131225
 BLAST score 301
 E value 3.0e-27
 Match length 93
 % identity 61
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 398137
 Seq. ID LIB3431-011-P1-K1-B2
 Method BLASTX
 NCBI GI g1621477
 BLAST score 378
 E value 2.0e-36
 Match length 81
 % identity 85
 NCBI Description (D85868) reverse transcriptase [Oryza sativa]

Seq. No. 398138
 Seq. ID LIB3431-011-P1-K1-B4
 Method BLASTX
 NCBI GI g5880709
 BLAST score 205
 E value 3.0e-16
 Match length 43
 % identity 100
 NCBI Description (AF137379) CF0 subunit III of ATP synthase [Nephroselmis olivacea]

Seq. No. 398139
 Seq. ID LIB3431-011-P1-K1-B5
 Method BLASTX
 NCBI GI g3850566
 BLAST score 263
 E value 7.0e-23
 Match length 134
 % identity 43
 NCBI Description (AC005278) F15K9.3 [Arabidopsis thaliana]

Seq. No. 398140
 Seq. ID LIB3431-011-P1-K1-B6
 Method BLASTN
 NCBI GI g218207
 BLAST score 294
 E value 1.0e-164
 Match length 298
 % identity 100
 NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398146
 Seq. ID LIB3431-011-P1-K1-C7
 Method BLASTX
 NCBI GI g133999
 BLAST score 493
 E value 7.0e-50
 Match length 100
 % identity 100
 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir_R3RZ7 ribosomal protein S7 - rice chloroplast >gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_226657_prf_1603356CH ribosomal protein S7 [Oryza sativa]

Seq. No. 398147
 Seq. ID LIB3431-011-P1-K1-C8
 Method BLASTX
 NCBI GI g2625084
 BLAST score 550
 E value 1.0e-56
 Match length 129
 % identity 85
 NCBI Description (AF030382) ADP-glucose pyrophosphorylase small subunit [Cucumis melo var. markuwa Markino]

Seq. No. 398148
 Seq. ID LIB3431-011-P1-K1-C9
 Method BLASTN
 NCBI GI g4574134
 BLAST score 123
 E value 6.0e-63
 Match length 146
 % identity 97
 NCBI Description Oryza sativa cysteine synthase (rcs1) mRNA, complete cds

Seq. No. 398149
 Seq. ID LIB3431-011-P1-K1-D1
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 1.0e-10
 Match length 49
 % identity 65
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398150
 Seq. ID LIB3431-011-P1-K1-D11
 Method BLASTX

```

NCBI GI      g2570505
BLAST score  242
E value      4.0e-27
Match length 87
% identity   83
NCBI Description (AF022735) proteasome component [Oryza sativa]

```

```
Seq. No.      398151
Seq. ID      LIB3431-011-P1-K1-D3
Method       BLASTN
NCBI GI      g3885891
BLAST score   110
E value      5.0e-55
Match length  181
% identity    97
NCBI Description  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                mRNA, complete cds
```

```
Seq. No.      398152
Seq. ID      LIB3431-011-P1-K1-D5
Method       BLASTX
NCBI GI      g5902394
BLAST score   440
E value      1.0e-43
Match length  114
% identity    76
NCBI Description (AC008148) Putative phosphoglucomutase [Arabidopsis thaliana]
```

Seq. No.	398153
Seq. ID	LIB3431-011-P1-K1-D7
Method	BLASTN
NCBI GI	g3810868
BLAST score	35
E value	8.0e-11
Match length	35
% identity	100
NCBI Description	Homo sapiens ST15 mRNA, complete cds

Seq. No.	398154
Seq. ID	LIB3431-011-P1-K1-D9
Method	BLASTX
NCBI GI	g2407281
BLAST score	543
E value	8.0e-56
Match length	105
% identity	95
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	398155
Seq. ID	LIB3431-011-P1-K1-E1
Method	BLASTX
NCBI GI	g4929595
BLAST score	239
E value	4.0e-20
Match length	102

000T0T"9T048960

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 398171
Seq. ID LIB3431-011-P1-K1-G2
Method BLASTN
NCBI GI g167086
BLAST score 43
E value 3.0e-15
Match length 74
% identity 90

NCBI Description Hordeum vulgare photosystem I protein (PSI-L) mRNA, complete cds

Seq. No. 398172
Seq. ID LIB3431-011-P1-K1-G4
Method BLASTX
NCBI GI g548605
BLAST score 570
E value 8.0e-59
Match length 124
% identity 91

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 398173
Seq. ID LIB3431-011-P1-K1-G5
Method BLASTX
NCBI GI g2499497
BLAST score 334
E value 5.0e-33
Match length 84
% identity 95

NCBI Description PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
>gi_1161600_emb_CAA88841_ (Z48977) phosphoglycerate kinase [Nicotiana tabacum]

Seq. No. 398174
Seq. ID LIB3431-011-P1-K1-G7
Method BLASTX
NCBI GI g2407281
BLAST score 513
E value 3.0e-52
Match length 109
% identity 90

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 398175
Seq. ID LIB3431-011-P1-K1-G9
Method BLASTX
NCBI GI g544437
BLAST score 323
E value 6.0e-30

Seq. No. 398181
 Seq. ID LIB3431-011-P1-K1-H4
 Method BLASTX
 NCBI GI g4886307
 BLAST score 704
 E value 1.0e-74
 Match length 135
 % identity 97
 NCBI Description (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase
 [Arabidopsis thaliana]

Seq. No. 398182
 Seq. ID LIB3431-011-P1-K1-H5
 Method BLASTX
 NCBI GI g3345477
 BLAST score 314
 E value 6.0e-29
 Match length 111
 % identity 58
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398183
 Seq. ID LIB3431-011-P1-K1-H7
 Method BLASTX
 NCBI GI g733458
 BLAST score 484
 E value 9.0e-49
 Match length 109
 % identity 84
 NCBI Description (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
 [Zea mays]

Seq. No. 398184
 Seq. ID LIB3431-011-P1-K1-H9
 Method BLASTX
 NCBI GI g320618
 BLAST score 386
 E value 1.0e-40
 Match length 116
 % identity 78
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 398185
 Seq. ID LIB3431-011-P1-N1-A1
 Method BLASTX
 NCBI GI g542157
 BLAST score 528
 E value 5.0e-54
 Match length 124
 % identity 85
 NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 398186

000001-010000

Seq. ID LIB3431-011-P1-N1-B2
 Method BLASTX
 NCBI GI g3377848
 BLAST score 198
 E value 3.0e-15
 Match length 95
 % identity 38
 NCBI Description (AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]

Seq. No. 398192
 Seq. ID LIB3431-011-P1-N1-B3
 Method BLASTX
 NCBI GI g6093830
 BLAST score 211
 E value 1.0e-16
 Match length 94
 % identity 34
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No. 398193
 Seq. ID LIB3431-011-P1-N1-B4
 Method BLASTN
 NCBI GI g11957
 BLAST score 341
 E value 0.0e+00
 Match length 362
 % identity 98
 NCBI Description Rice complete chloroplast genome

Seq. No. 398194
 Seq. ID LIB3431-011-P1-N1-B5
 Method BLASTX
 NCBI GI g3924605
 BLAST score 251
 E value 2.0e-21
 Match length 59
 % identity 71
 NCBI Description (AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]

Seq. No. 398195
 Seq. ID LIB3431-011-P1-N1-B6
 Method BLASTN
 NCBI GI g218207
 BLAST score 298
 E value 1.0e-167
 Match length 298
 % identity 100
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone poSSS1139

Seq. No. 398196

Seq. ID LIB3431-011-P1-N1-B9
 Method BLASTX
 NCBI GI g421855
 BLAST score 151
 E value 1.0e-09
 Match length 79
 % identity 44
 NCBI Description alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No. 398197
 Seq. ID LIB3431-011-P1-N1-C10
 Method BLASTX
 NCBI GI g3929924
 BLAST score 163
 E value 3.0e-11
 Match length 36
 % identity 89
 NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 398198
 Seq. ID LIB3431-011-P1-N1-C3
 Method BLASTX
 NCBI GI g1504052
 BLAST score 270
 E value 1.0e-23
 Match length 52
 % identity 100
 NCBI Description (D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No. 398199
 Seq. ID LIB3431-011-P1-N1-C5
 Method BLASTX
 NCBI GI g289920
 BLAST score 217
 E value 1.0e-17
 Match length 42
 % identity 98
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 398200
 Seq. ID LIB3431-011-P1-N1-C6
 Method BLASTX
 NCBI GI g132105
 BLAST score 289
 E value 8.0e-26
 Match length 73
 % identity 78
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate

05684016707000

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Seq. No.      398202
Seq. ID      LIB3431-011-P1-N1-C9
Method       BLASTN
NCBI GI      g4574134
BLAST score   147
E value      3.0e-77
Match length  147
% identity    100
NCBI Description  Oryza sativa cysteine synthase (rcs1) mRNA, complete cds
```

```
Seq. No.      398204
Seq. ID      LIB3431-011-P1-N1-D3
Method       BLASTX
NCBI GI      g3885892
BLAST score   426
E value      6.0e-42
Match length  83
% identity   98
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
```

Seq. No.	398206
Seq. ID	LIB3431-011-P1-N1-D9
Method	BLASTN

09684015-101000

NCBI GI g218209
BLAST score 149
E value 4.0e-78
Match length 299
% identity 97
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 398207
Seq. ID LIB3431-011-P1-N1-E12
Method BLASTX
NCBI GI g115802
BLAST score 217
E value 1.0e-17
Match length 40
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
>gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No. 398208
Seq. ID LIB3431-011-P1-N1-E3
Method BLASTX
NCBI GI g417260
BLAST score 326
E value 3.0e-30
Match length 81
% identity 77
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No. 398209
Seq. ID LIB3431-011-P1-N1-E5
Method BLASTX
NCBI GI g517500
BLAST score 234
E value 1.0e-19
Match length 79
% identity 62
NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 398210
Seq. ID LIB3431-011-P1-N1-E9
Method BLASTX
NCBI GI g3212877
BLAST score 180
E value 3.0e-13
Match length 40
% identity 85
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]

E value 3.0e-09
 Match length 30
 % identity 87
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
 >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No. 398216
 Seq. ID LIB3431-011-P1-N1-F8
 Method BLASTX
 NCBI GI g3036949
 BLAST score 264
 E value 4.0e-23
 Match length 50
 % identity 100
 NCBI Description (AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 398217
 Seq. ID LIB3431-011-P1-N1-F9
 Method BLASTX
 NCBI GI g1076678
 BLAST score 243
 E value 1.0e-20
 Match length 48
 % identity 100
 NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 398218
 Seq. ID LIB3431-011-P1-N1-G1
 Method BLASTX
 NCBI GI g131176
 BLAST score 304
 E value 1.0e-27
 Match length 59
 % identity 98
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
 >gi_72683_pir_F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No. 398219
 Seq. ID LIB3431-011-P1-N1-G12
 Method BLASTN
 NCBI GI g3789951
 BLAST score 191
 E value 1.0e-103
 Match length 414
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 398220
 Seq. ID LIB3431-011-P1-N1-G2
 Method BLASTX
 NCBI GI g6006283
 BLAST score 151
 E value 8.0e-10
 Match length 41
 % identity 73
 NCBI Description (AB015861) photosystem I subunit PSI-L [Arabidopsis thaliana]

Seq. No. 398221
 Seq. ID LIB3431-011-P1-N1-G4
 Method BLASTX
 NCBI GI g548605
 BLAST score 402
 E value 9.0e-40
 Match length 105
 % identity 87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 398222
 Seq. ID LIB3431-011-P1-N1-G5
 Method BLASTX
 NCBI GI g3738261
 BLAST score 416
 E value 9.0e-41
 Match length 91
 % identity 92
 NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No. 398223
 Seq. ID LIB3431-011-P1-N1-G9
 Method BLASTX
 NCBI GI g485512
 BLAST score 326
 E value 3.0e-30
 Match length 70
 % identity 87
 NCBI Description salt-associated protein csaA - sweet orange

Seq. No. 398224
 Seq. ID LIB3431-011-P1-N1-H10
 Method BLASTX
 NCBI GI g2754849
 BLAST score 186
 E value 7.0e-14
 Match length 43
 % identity 84
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

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NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398235
 Seq. ID LIB3431-012-P1-K1-B10
 Method BLASTN
 NCBI GI g6015437
 BLAST score 35
 E value 2.0e-10
 Match length 35
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398236
 Seq. ID LIB3431-012-P1-K1-B11
 Method BLASTN
 NCBI GI g6015437
 BLAST score 43
 E value 4.0e-15
 Match length 43
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398237
 Seq. ID LIB3431-012-P1-K1-B12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 221
 E value 6.0e-18
 Match length 44
 % identity 93
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 398238
 Seq. ID LIB3431-012-P1-K1-B3
 Method BLASTX
 NCBI GI g4836934
 BLAST score 187
 E value 7.0e-14
 Match length 86
 % identity 43
 NCBI Description (AC006085) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 398239
 Seq. ID LIB3431-012-P1-K1-B4
 Method BLASTN
 NCBI GI g218207
 BLAST score 253
 E value 1.0e-140
 Match length 257
 % identity 100
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS1139

Seq. No. 398240

Seq. ID LIB3431-012-P1-K1-B5
 Method BLASTN
 NCBI GI g3789951
 BLAST score 62
 E value 3.0e-26
 Match length 121
 % identity 88
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor
 (Cab27) mRNA, nuclear gene encoding chloroplast protein,
 complete cds

Seq. No. 398241
 Seq. ID LIB3431-012-P1-K1-B6
 Method BLASTX
 NCBI GI g3075488
 BLAST score 211
 E value 3.0e-17
 Match length 59
 % identity 69
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 398242
 Seq. ID LIB3431-012-P1-K1-B8
 Method BLASTX
 NCBI GI g548603
 BLAST score 380
 E value 1.0e-36
 Match length 120
 % identity 68
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
 barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 398243
 Seq. ID LIB3431-012-P1-K1-B9
 Method BLASTX
 NCBI GI g131225
 BLAST score 378
 E value 1.0e-36
 Match length 85
 % identity 88
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 398244
 Seq. ID LIB3431-012-P1-K1-C1
 Method BLASTX
 NCBI GI g1707018
 BLAST score 460
 E value 7.0e-46
 Match length 104
 % identity 86
 NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]

Seq. No. 398245
 Seq. ID LIB3431-012-P1-K1-C11
 Method BLASTX
 NCBI GI g2244867
 BLAST score 298
 E value 6.0e-27
 Match length 137
 % identity 44
 NCBI Description (Z97337) hydroxynitrile lyase like protein [Arabidopsis thaliana]

Seq. No. 398246
 Seq. ID LIB3431-012-P1-K1-C2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 208
 E value 3.0e-16
 Match length 62
 % identity 63
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398247
 Seq. ID LIB3431-012-P1-K1-C3
 Method BLASTX
 NCBI GI g4079798
 BLAST score 223
 E value 2.0e-18
 Match length 46
 % identity 96
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 398248
 Seq. ID LIB3431-012-P1-K1-C4
 Method BLASTX
 NCBI GI g2407281
 BLAST score 304
 E value 1.0e-27
 Match length 87
 % identity 68
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 398249
 Seq. ID LIB3431-012-P1-K1-C5
 Method BLASTX
 NCBI GI g1353352
 BLAST score 423
 E value 2.0e-41
 Match length 116
 % identity 72
 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 398250

Seq. ID LIB3431-012-P1-K1-C7
Method BLASTN
NCBI GI g1944204
BLAST score 451
E value 0.0e+00
Match length 466
% identity 99
NCBI Description Oryza sativa mRNA for RicMT, complete cds

Seq. No. 398251
Seq. ID LIB3431-012-P1-K1-C8
Method BLASTX
NCBI GI g4585142
BLAST score 388
E value 2.0e-37
Match length 101
% identity 71
NCBI Description (AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon
esculentum]

Seq. No. 398252
Seq. ID LIB3431-012-P1-K1-C9
Method BLASTX
NCBI GI g170131
BLAST score 176
E value 1.0e-12
Match length 48
% identity 62
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 398253
Seq. ID LIB3431-012-P1-K1-D1
Method BLASTX
NCBI GI g5091623
BLAST score 521
E value 5.0e-53
Match length 125
% identity 82
NCBI Description (AC007454) Similar to gb_U93048 somatic embryogenesis
receptor-like kinase from Daucus carota, contains 4
PF_00560 Leucine Rich Repeat domains and a PF_00069
Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No. 398254
Seq. ID LIB3431-012-P1-K1-D10
Method BLASTX
NCBI GI g4510363
BLAST score 511
E value 6.0e-52
Match length 123
% identity 80
NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
thaliana]

Seq. No. 398255
Seq. ID LIB3431-012-P1-K1-D12
Method BLASTX

NCBI GI g6056373
 BLAST score 218
 E value 1.0e-19
 Match length 102
 % identity 59
 NCBI Description (AC009894) elongation factor EF-2 [Arabidopsis thaliana]

Seq. No. 398256
 Seq. ID LIB3431-012-P1-K1-D2
 Method BLASTX
 NCBI GI g733454
 BLAST score 575
 E value 2.0e-59
 Match length 133
 % identity 82
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 398257
 Seq. ID LIB3431-012-P1-K1-D4
 Method BLASTN
 NCBI GI g20239
 BLAST score 119
 E value 4.0e-60
 Match length 135
 % identity 97
 NCBI Description O.sativa (rice) shoot-specific GOS5 gene for a putative chloroplast transit peptide

Seq. No. 398258
 Seq. ID LIB3431-012-P1-K1-D6
 Method BLASTX
 NCBI GI g1055130
 BLAST score 220
 E value 8.0e-18
 Match length 131
 % identity 44
 NCBI Description (U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No. 398259
 Seq. ID LIB3431-012-P1-K1-D8
 Method BLASTX
 NCBI GI g3522929
 BLAST score 589
 E value 5.0e-61
 Match length 126
 % identity 87
 NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 398260
 Seq. ID LIB3431-012-P1-K1-D9

Method BLASTX
 NCBI GI g115787
 BLAST score 365
 E value 4.0e-35
 Match length 94
 % identity 81
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398261
 Seq. ID LIB3431-012-P1-K1-E10
 Method BLASTX
 NCBI GI g115794
 BLAST score 787
 E value 3.0e-84
 Match length 156
 % identity 93
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No. 398262
 Seq. ID LIB3431-012-P1-K1-E11
 Method BLASTX
 NCBI GI g4239891
 BLAST score 617
 E value 3.0e-67
 Match length 151
 % identity 87
 NCBI Description (AB016804) NADP-malic enzyme [Aloe arborescens]

Seq. No. 398263
 Seq. ID LIB3431-012-P1-K1-E12
 Method BLASTX
 NCBI GI g115787
 BLAST score 352
 E value 2.0e-33
 Match length 90
 % identity 80
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398264
 Seq. ID LIB3431-012-P1-K1-E4
 Method BLASTX
 NCBI GI g4531444
 BLAST score 472
 E value 3.0e-47
 Match length 148

Seq. No. 398275
 Seq. ID LIB3431-012-P1-K1-G2
 Method BLASTX
 NCBI GI g115525
 BLAST score 162
 E value 8.0e-19
 Match length 78
 % identity 67
 NCBI Description CALMODULIN >gi_71685_pir_MCSP calmodulin - spinach

Seq. No. 398276
 Seq. ID LIB3431-012-P1-K1-G3
 Method BLASTX
 NCBI GI g1709846
 BLAST score 226
 E value 2.0e-18
 Match length 133
 % identity 38
 NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
 22 kDa component of photosystem II [Lycopersicon
 esculentum]

Seq. No. 398277
 Seq. ID LIB3431-012-P1-K1-G5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 626
 E value 2.0e-65
 Match length 128
 % identity 91
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 398278
 Seq. ID LIB3431-012-P1-K1-G6
 Method BLASTX
 NCBI GI g1353352
 BLAST score 342
 E value 5.0e-32
 Match length 104
 % identity 63
 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
 reinhardtii]

Seq. No. 398279
 Seq. ID LIB3431-012-P1-K1-G7
 Method BLASTX
 NCBI GI g122106
 BLAST score 389
 E value 1.0e-37
 Match length 79
 % identity 99
 NCBI Description HISTONE H4 >gi_70771_pir_HSZM4 histone H4 - maize
 >gi_81642_pir_S06904 histone H4 - Arabidopsis thaliana
 >gi_2119028_pir_S60475 histone H4 - garden pea
 >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum

aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf_1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 398280
Seq. ID LIB3431-012-P1-K1-G9
Method BLASTX
NCBI GI g3075382
BLAST score 212
E value 7.0e-17
Match length 110
% identity 50
NCBI Description (AC002505) putative peroxisome assembly protein PER8 [Arabidopsis thaliana] >gi_3075384 (AC004484) putative peroxisome assembly protein PER8 [Arabidopsis thaliana]

Seq. No. 398281
Seq. ID LIB3431-012-P1-K1-H1
Method BLASTX
NCBI GI g3355477
BLAST score 441
E value 1.0e-43
Match length 105
% identity 44
NCBI Description (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No. 398282
Seq. ID LIB3431-012-P1-K1-H10
Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 1.0e-11
Match length 36
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398283
Seq. ID LIB3431-012-P1-K1-H2
Method BLASTX
NCBI GI g4102703
BLAST score 468
E value 1.0e-52
Match length 140
% identity 79
NCBI Description (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No. 398284
 Seq. ID LIB3431-012-P1-K1-H3
 Method BLASTX
 NCBI GI g2653558
 BLAST score 776
 E value 6.0e-83
 Match length 159
 % identity 91
 NCBI Description (D50679) ferredoxin-sulfite reductase precursor [Zea mays]

Seq. No. 398285
 Seq. ID LIB3431-012-P1-K1-H5
 Method BLASTX
 NCBI GI g2982453
 BLAST score 295
 E value 4.0e-27
 Match length 63
 % identity 94
 NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No. 398286
 Seq. ID LIB3431-012-P1-K1-H7
 Method BLASTX
 NCBI GI g115787
 BLAST score 280
 E value 3.0e-25
 Match length 77
 % identity 77
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398287
 Seq. ID LIB3431-012-P1-K1-H8
 Method BLASTX
 NCBI GI g3345477
 BLAST score 429
 E value 3.0e-42
 Match length 128
 % identity 68
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398288
 Seq. ID LIB3431-012-P1-K1-H9
 Method BLASTN
 NCBI GI g4887617
 BLAST score 131
 E value 2.0e-67
 Match length 142
 % identity 98
 NCBI Description Oryza sativa HOS59 mRNA, partial cds

Seq. No. 398289
 Seq. ID LIB3431-013-P1-K1-A10

Method BLASTX
NCBI GI g2673914
BLAST score 325
E value 8.0e-42
Match length 139
% identity 62
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398290
Seq. ID LIB3431-013-P1-K1-A12
Method BLASTX
NCBI GI g2660669
BLAST score 311
E value 2.0e-28
Match length 131
% identity 47
NCBI Description (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]

Seq. No. 398291
Seq. ID LIB3431-013-P1-K1-A4
Method BLASTX
NCBI GI g132105
BLAST score 417
E value 5.0e-43
Match length 130
% identity 76
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398292
Seq. ID LIB3431-013-P1-K1-A5
Method BLASTX
NCBI GI g4206195
BLAST score 213
E value 5.0e-17
Match length 54
% identity 67
NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398293
Seq. ID LIB3431-013-P1-K1-A6
Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398294
Seq. ID LIB3431-013-P1-K1-A8
Method BLASTN
NCBI GI g4959460
BLAST score 35
E value 5.0e-10
Match length 35
% identity 100

NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 398295
Seq. ID LIB3431-013-P1-K1-A9
Method BLASTX
NCBI GI g2894534
BLAST score 537
E value 5.0e-55
Match length 116
% identity 91
NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 398296
Seq. ID LIB3431-013-P1-K1-B1
Method BLASTX
NCBI GI g1835731
BLAST score 348
E value 4.0e-33
Match length 69
% identity 99
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 398297
Seq. ID LIB3431-013-P1-K1-B10
Method BLASTX
NCBI GI g479406
BLAST score 649
E value 4.0e-68
Match length 126
% identity 94
NCBI Description chlorophyll a/b-binding protein - garden pea
>gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
protein [Pisum sativum]

Seq. No. 398298
Seq. ID LIB3431-013-P1-K1-B11
Method BLASTX
NCBI GI g320618
BLAST score 407
E value 9.0e-40
Match length 89
% identity 93
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 398299
 Seq. ID LIB3431-013-P1-K1-B12
 Method BLASTX
 NCBI GI g1169798
 BLAST score 336
 E value 2.0e-31
 Match length 85
 % identity 79
 NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)
 (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
 ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218)
 phosphoglucose isomerase (Pgi-b) [Oryza sativa]

Seq. No. 398300
 Seq. ID LIB3431-013-P1-K1-B2
 Method BLASTX
 NCBI GI g132105
 BLAST score 501
 E value 1.0e-52
 Match length 134
 % identity 81
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor. (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398301
 Seq. ID LIB3431-013-P1-K1-B3
 Method BLASTN
 NCBI GI g6002093
 BLAST score 52
 E value 9.0e-21
 Match length 63
 % identity 97
 NCBI Description Zizania latifolia chloroplast rps4 gene for ribosomal
 protein S4

Seq. No. 398302
 Seq. ID LIB3431-013-P1-K1-B4
 Method BLASTX
 NCBI GI g488573
 BLAST score 600
 E value 2.0e-62
 Match length 122
 % identity 98
 NCBI Description (U09463) histone H3.2 [Medicago sativa]

Seq. No. 398303
 Seq. ID LIB3431-013-P1-K1-B7
 Method BLASTX
 NCBI GI g3757521

Match length 138
 % identity 99
 NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR
 (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31)
 >gi_68598_pir_AJRZQD glutamate--ammonia ligase (EC
 6.3.1.2) delta precursor, chloroplast - rice
 >gi_20370_emb_CAA32462_ (X14246) precursor chloroplastic
 glutamine synthetase (AA -46 to 382) [Oryza sativa]

Seq. No. 398314
 Seq. ID LIB3431-013-P1-K1-D11
 Method BLASTX
 NCBI GI g3789952
 BLAST score 566
 E value 1.0e-58
 Match length 127
 % identity 94
 NCBI Description (AF094775) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 398315
 Seq. ID LIB3431-013-P1-K1-D12
 Method BLASTX
 NCBI GI g3913240
 BLAST score 401
 E value 5.0e-39
 Match length 94
 % identity 90
 NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR
 (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D)
 >gi_2239151_emb_CAA71128_ (Y10022) CHLD magnesium chelatase
 subunit [Nicotiana tabacum]

Seq. No. 398316
 Seq. ID LIB3431-013-P1-K1-D2
 Method BLASTX
 NCBI GI g132105
 BLAST score 178
 E value 2.0e-13
 Match length 55
 % identity 67
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398317
 Seq. ID LIB3431-013-P1-K1-D3
 Method BLASTX
 NCBI GI g82080
 BLAST score 383
 E value 6.0e-37

Match length 107
 % identity 67
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 398318
 Seq. ID LIB3431-013-P1-K1-D5
 Method BLASTX
 NCBI GI g417260
 BLAST score 421
 E value 2.0e-41
 Match length 128
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 398319
 Seq. ID LIB3431-013-P1-K1-D9
 Method BLASTX
 NCBI GI g100615
 BLAST score 732
 E value 8.0e-78
 Match length 143
 % identity 96
 NCBI Description ribulose-bisphosphate carboxylase activase A short form
 precursor - barley >gi_167091 (M55447) ribulose
 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No. 398320
 Seq. ID LIB3431-013-P1-K1-E1
 Method BLASTX
 NCBI GI g671740
 BLAST score 558
 E value 2.0e-57
 Match length 107
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 398321
 Seq. ID LIB3431-013-P1-K1-E10
 Method BLASTX
 NCBI GI g3126854
 BLAST score 705
 E value 1.0e-74
 Match length 133
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398322
 Seq. ID LIB3431-013-P1-K1-E11
 Method BLASTX
 NCBI GI g115787
 BLAST score 699
 E value 6.0e-74

activase [Oryza sativa]

Seq. No. 398332
 Seq. ID LIB3431-013-P1-K1-F2
 Method BLASTX
 NCBI GI g2290681
 BLAST score 178
 E value 7.0e-25
 Match length 145
 % identity 46
 NCBI Description (AF000135) acidic cellulase [Citrus sinensis]

Seq. No. 398333
 Seq. ID LIB3431-013-P1-K1-F3
 Method BLASTX
 NCBI GI g1777312
 BLAST score 382
 E value 8.0e-37
 Match length 108
 % identity 66
 NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 398334
 Seq. ID LIB3431-013-P1-K1-F7
 Method BLASTX
 NCBI GI g1729971
 BLAST score 327
 E value 2.0e-30
 Match length 99
 % identity 69
 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa]

Seq. No. 398335
 Seq. ID LIB3431-013-P1-K1-F8
 Method BLASTX
 NCBI GI g4079798
 BLAST score 293
 E value 2.0e-26
 Match length 104
 % identity 59
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 398336
 Seq. ID LIB3431-013-P1-K1-G1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 228
 E value 1.0e-18
 Match length 44
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 398337
 Seq. ID LIB3431-013-P1-K1-G3
 Method BLASTX
 NCBI GI g347451
 BLAST score 536
 E value 7.0e-55
 Match length 117
 % identity 86
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 398338
 Seq. ID LIB3431-013-P1-K1-G4
 Method BLASTX
 NCBI GI g132105
 BLAST score 665
 E value 6.0e-70
 Match length 144
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398339
 Seq. ID LIB3431-013-P1-K1-G6
 Method BLASTN
 NCBI GI g20262
 BLAST score 157
 E value 4.0e-83
 Match length 187
 % identity 96
 NCBI Description O.sativa light-induced mRNA

Seq. No. 398340
 Seq. ID LIB3431-013-P1-K1-G8
 Method BLASTX
 NCBI GI g729668
 BLAST score 245
 E value 6.0e-21
 Match length 83
 % identity 55
 NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 398341
 Seq. ID LIB3431-013-P1-K1-G9
 Method BLASTX
 NCBI GI g4469021

BLAST score 245
 E value 1.0e-20
 Match length 72
 % identity 69
 NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398342
 Seq. ID LIB3431-013-P1-K1-H1
 Method BLASTN
 NCBI GI g3041776
 BLAST score 60
 E value 2.0e-25
 Match length 88
 % identity 92
 NCBI Description Oryza sativa mRNA for fructose-1,6-bisphosphatase (plastidic isoform), complete cds

Seq. No. 398343
 Seq. ID LIB3431-013-P1-K1-H11
 Method BLASTX
 NCBI GI g3789954
 BLAST score 368
 E value 4.0e-35
 Match length 110
 % identity 68
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398344
 Seq. ID LIB3431-013-P1-K1-H12
 Method BLASTX
 NCBI GI g4079798
 BLAST score 376
 E value 5.0e-36
 Match length 125
 % identity 62
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 398345
 Seq. ID LIB3431-013-P1-K1-H3
 Method BLASTN
 NCBI GI g2072554
 BLAST score 102
 E value 2.0e-50
 Match length 118
 % identity 97
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 398346
 Seq. ID LIB3431-013-P1-K1-H5
 Method BLASTX
 NCBI GI g2586083
 BLAST score 206
 E value 2.0e-17
 Match length 117

% identity 86
 NCBI Description (AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No. 398356
 Seq. ID LIB3431-014-P1-K1-B12
 Method BLASTX
 NCBI GI g1001794
 BLAST score 161
 E value 4.0e-11
 Match length 41
 % identity 71
 NCBI Description (D64005) hypothetical protein [Synechocystis sp.]

Seq. No. 398357
 Seq. ID LIB3431-014-P1-K1-B2
 Method BLASTN
 NCBI GI g5478796
 BLAST score 57
 E value 1.0e-23
 Match length 73
 % identity 96
 NCBI Description Oryza sativa CAO mRNA for chlorophyll b synthase, partial cds

Seq. No. 398358
 Seq. ID LIB3431-014-P1-K1-B3
 Method BLASTN
 NCBI GI g19094
 BLAST score 46
 E value 6.0e-17
 Match length 54
 % identity 96
 NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No. 398359
 Seq. ID LIB3431-014-P1-K1-B6
 Method BLASTX
 NCBI GI g4741205
 BLAST score 395
 E value 2.0e-38
 Match length 107
 % identity 64
 NCBI Description (AL049746) putative protein [Arabidopsis thaliana]

Seq. No. 398360
 Seq. ID LIB3431-014-P1-K1-B8
 Method BLASTX
 NCBI GI g1262849
 BLAST score 266
 E value 1.0e-25
 Match length 64
 % identity 95
 NCBI Description (U51633) type 1 light-harvesting chlorophyll a/b-binding polypeptide [Pinus palustris]

Seq. No. 398361

Seq. ID LIB3431-014-P1-K1-C1
 Method BLASTN
 NCBI GI g3063523
 BLAST score 45
 E value 6.0e-17
 Match length 49
 % identity 98
 NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 398362
 Seq. ID LIB3431-014-P1-K1-C10
 Method BLASTN
 NCBI GI g3885891
 BLAST score 41
 E value 5.0e-14
 Match length 85
 % identity 87
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 398363
 Seq. ID LIB3431-014-P1-K1-C11
 Method BLASTX
 NCBI GI g3122914
 BLAST score 213
 E value 6.0e-17
 Match length 147
 % identity 31
 NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
 >gi_1890130_gb_AAB49704.1_ (U89986) valyl tRNA synthetase
 [Arabidopsis thaliana]

Seq. No. 398364
 Seq. ID LIB3431-014-P1-K1-C2
 Method BLASTX
 NCBI GI g3126854
 BLAST score 609
 E value 2.0e-63
 Match length 119
 % identity 96
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398365
 Seq. ID LIB3431-014-P1-K1-C7
 Method BLASTN
 NCBI GI g3126853
 BLAST score 172
 E value 7.0e-92
 Match length 210
 % identity 100
 NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 398366
 Seq. ID LIB3431-014-P1-K1-C8

09684016.101000

Match length	140
% identity	94
NCBI Description	(U19183) acetyl-coenzyme A carboxylase [Zea mays]
Seq. No.	398372
Seq. ID	LIB3431-014-P1-K1-D3
Method	BLASTX
NCBI GI	g2306981
BLAST score	480
E value	4.0e-48
Match length	101
% identity	83
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.	398373
Seq. ID	LIB3431-014-P1-K1-D4
Method	BLASTN
NCBI GI	g1835730
BLAST score	73
E value	8.0e-33
Match length	89
% identity	96
NCBI Description	Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds
Seq. No.	398374
Seq. ID	LIB3431-014-P1-K1-D5
Method	BLASTX
NCBI GI	g2160322
BLAST score	281
E value	5.0e-25
Match length	66
% identity	85
NCBI Description	(D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]
Seq. No.	398375
Seq. ID	LIB3431-014-P1-K1-D9
Method	BLASTX
NCBI GI	g132105
BLAST score	304
E value	1.0e-27
Match length	78
% identity	79
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	398376
Seq. ID	LIB3431-014-P1-K1-E1
Method	BLASTX

NCBI GI g3914603
 BLAST score 664
 E value 6.0e-70
 Match length 130
 % identity 97
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
 activase [Oryza sativa]

Seq. No. 398377
 Seq. ID LIB3431-014-P1-K1-E10
 Method BLASTX
 NCBI GI g3025189
 BLAST score 455
 E value 3.0e-45
 Match length 141
 % identity 61
 NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770
 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis
 sp.]

Seq. No. 398378
 Seq. ID LIB3431-014-P1-K1-E11
 Method BLASTX
 NCBI GI g2894534
 BLAST score 746
 E value 2.0e-79
 Match length 146
 % identity 99
 NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 398379
 Seq. ID LIB3431-014-P1-K1-E12
 Method BLASTX
 NCBI GI g3345477
 BLAST score 534
 E value 1.0e-54
 Match length 149
 % identity 70
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398380
 Seq. ID LIB3431-014-P1-K1-E2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 398381
 Seq. ID LIB3431-014-P1-K1-E4
 Method BLASTX

09634015-101000

BLAST score 608
 E value 3.0e-63
 Match length 133
 % identity 91
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 398387
 Seq. ID LIB3431-014-P1-K1-F10
 Method BLASTX
 NCBI GI g3548815
 BLAST score 254
 E value 1.0e-21
 Match length 109
 % identity 50
 NCBI Description (AC005313) similar to axoneme-associated protein mst101
 [Arabidopsis thaliana]

Seq. No. 398388
 Seq. ID LIB3431-014-P1-K1-F11
 Method BLASTX
 NCBI GI g1903364
 BLAST score 296
 E value 1.0e-26
 Match length 145
 % identity 43
 NCBI Description (AC000104) EST gb_T45093 comes from this gene. [Arabidopsis
 thaliana]

Seq. No. 398389
 Seq. ID LIB3431-014-P1-K1-F2
 Method BLASTX
 NCBI GI g3738285
 BLAST score 320
 E value 2.0e-29
 Match length 101
 % identity 61
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 398390
 Seq. ID LIB3431-014-P1-K1-F4
 Method BLASTX
 NCBI GI g3548815
 BLAST score 255
 E value 6.0e-22
 Match length 105
 % identity 48
 NCBI Description (AC005313) similar to axoneme-associated protein mst101
 [Arabidopsis thaliana]

Seq. No. 398391
 Seq. ID LIB3431-014-P1-K1-F6
 Method BLASTX
 NCBI GI g1346771

```

BLAST score          778
E value              4.0e-83
Match length         158
% identity            91
NCBI Description     PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
                    >gi_1086117_pir_S52988 phosphoenolpyruvate carboxykinase
                    (PCK1) - Urochloa panicoides >gi_607752 (U09241)
                    phosphoenolpyruvate carboxykinase [Urochloa panicoides]

Seq. No.             398392
Seq. ID              LIB3431-014-P1-K1-F9
Method               BLASTX
NCBI GI              g3789954
BLAST score          328
E value              7.0e-31
Match length         66
% identity            94
NCBI Description     (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                    sativa]

Seq. No.             398393
Seq. ID              LIB3431-014-P1-K1-G1
Method               BLASTX
NCBI GI              g2501189
BLAST score          464
E value              1.0e-46
Match length         101
% identity            88
NCBI Description     THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                    >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
                    - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                    [Zea mays]

Seq. No.             398394
Seq. ID              LIB3431-014-P1-K1-G10
Method               BLASTX
NCBI GI              g2626753
BLAST score          376
E value              4.0e-36
Match length         109
% identity            67
NCBI Description     (AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No.             398395
Seq. ID              LIB3431-014-P1-K1-G12
Method               BLASTX
NCBI GI              g1769887
BLAST score          456
E value              1.0e-45
Match length         110
% identity            76
NCBI Description     (X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.             398396
Seq. ID              LIB3431-014-P1-K1-G2
Method               BLASTX
NCBI GI              q3913018

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E value 5.0e-28
Match length 80
% identity 98
NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
clone:Aldp

Seq. No. 398411
Seq. ID LIB3431-014-P1-N1-B10
Method BLASTX
NCBI GI g347451
BLAST score 207
E value 2.0e-16
Match length 39
% identity 100
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
sativa]

Seq. No. 398412
Seq. ID LIB3431-014-P1-N1-B12
Method BLASTX
NCBI GI g1001794
BLAST score 168
E value 6.0e-12
Match length 41
% identity 73
NCBI Description (D64005) hypothetical protein [Synechocystis sp.]

Seq. No. 398413
Seq. ID LIB3431-014-P1-N1-B3
Method BLASTX
NCBI GI g3914466
BLAST score 302
E value 2.0e-27
Match length 71
% identity 79
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
(PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
subunit precursor [Zea mays]

Seq. No. 398414
Seq. ID LIB3431-014-P1-N1-B8
Method BLASTN
NCBI GI g20181
BLAST score 138
E value 1.0e-71
Match length 145
% identity 99
NCBI Description Rice cab2R gene for light harvesting chlorophyll
a/b-binding protein

Seq. No. 398415
Seq. ID LIB3431-014-P1-N1-C1
Method BLASTN
NCBI GI g218207
BLAST score 94
E value 1.0e-45
Match length 138

% identity	92
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139
Seq. No.	398416
Seq. ID	LIB3431-014-P1-N1-C10
Method	BLASTX
NCBI GI	g3885892
BLAST score	342
E value	4.0e-32
Match length	66
% identity	100
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.	398417
Seq. ID	LIB3431-014-P1-N1-C2
Method	BLASTX
NCBI GI	g3126854
BLAST score	272
E value	6.0e-24
Match length	57
% identity	93
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	398418
Seq. ID	LIB3431-014-P1-N1-C7
Method	BLASTN
NCBI GI	g3126853
BLAST score	145
E value	8.0e-76
Match length	207
% identity	97
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	398419
Seq. ID	LIB3431-014-P1-N1-C8
Method	BLASTX
NCBI GI	g3126854
BLAST score	456
E value	9.0e-46
Match length	103
% identity	94
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	398420
Seq. ID	LIB3431-014-P1-N1-D10
Method	BLASTX
NCBI GI	g1835731
BLAST score	236
E value	6.0e-20
Match length	56
% identity	82
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 398421
 Seq. ID LIB3431-014-P1-N1-D11
 Method BLASTX
 NCBI GI g733454
 BLAST score 210
 E value 1.0e-16
 Match length 48
 % identity 85
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 398422
 Seq. ID LIB3431-014-P1-N1-D3
 Method BLASTX
 NCBI GI g99486
 BLAST score 275
 E value 4.0e-24
 Match length 67
 % identity 79
 NCBI Description chlorophyll a/b-binding protein (clone pINEab 31) - Scotch pine >gi_20792_emb_CAA41406_ (X58516) Type II chlorophyll a/b-binding protein [Pinus sylvestris]

Seq. No. 398423
 Seq. ID LIB3431-014-P1-N1-D6
 Method BLASTN
 NCBI GI g168525
 BLAST score 37
 E value 3.0e-11
 Match length 53
 % identity 92
 NCBI Description Zea mays nucleic acid-binding protein (NBP)

Seq. No. 398424
 Seq. ID LIB3431-014-P1-N1-D8
 Method BLASTX
 NCBI GI g80783
 BLAST score 190
 E value 3.0e-14
 Match length 120
 % identity 36
 NCBI Description hypothetical 31.7K protein (aphE region) - Streptomyces griseus >gi_153164 (M37378) streptomycin-3'-phosphotransferase [Streptomyces griseus]

Seq. No. 398425
 Seq. ID LIB3431-014-P1-N1-D9
 Method BLASTX
 NCBI GI g671740
 BLAST score 225
 E value 2.0e-18
 Match length 44
 % identity 98
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 398426

Seq. ID LIB3431-014-P1-N1-E1
 Method BLASTX
 NCBI GI g132166
 BLAST score 149
 E value 1.0e-09
 Match length 31
 % identity 81
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
 activase precursor - Arabidopsis thaliana
 >gi_16471_emb_CAA32429 (X14212) rubisco activase (AA 1 -
 473) [Arabidopsis thaliana]

Seq. No. 398427
 Seq. ID LIB3431-014-P1-N1-E11
 Method BLASTX
 NCBI GI g2696804
 BLAST score 308
 E value 4.0e-28
 Match length 56
 % identity 100
 NCBI Description (AB009665) water channel protein [Oryza sativa]

Seq. No. 398428
 Seq. ID LIB3431-014-P1-N1-E12
 Method BLASTN
 NCBI GI g606816
 BLAST score 350
 E value 0.0e+00
 Match length 364
 % identity 99
 NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete
 cds

Seq. No. 398429
 Seq. ID LIB3431-014-P1-N1-E2
 Method BLASTN
 NCBI GI g2072554
 BLAST score 343
 E value 0.0e+00
 Match length 377
 % identity 98
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 398430
 Seq. ID LIB3431-014-P1-N1-E4
 Method BLASTX
 NCBI GI g3036951
 BLAST score 233
 E value 2.0e-19
 Match length 57
 % identity 93
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [Nicotiana glauca]

Seq. No. 398431
 Seq. ID LIB3431-014-P1-N1-E5
 Method BLASTX
 NCBI GI g3808101
 BLAST score 181
 E value 2.0e-13
 Match length 43
 % identity 84
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 398432
 Seq. ID LIB3431-014-P1-N1-E8
 Method BLASTX
 NCBI GI g2407279
 BLAST score 200
 E value 8.0e-25
 Match length 67
 % identity 93
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 398433
 Seq. ID LIB3431-014-P1-N1-E9
 Method BLASTX
 NCBI GI g2982362
 BLAST score 494
 E value 6.0e-50
 Match length 100
 % identity 89
 NCBI Description (AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No. 398434
 Seq. ID LIB3431-014-P1-N1-F1
 Method BLASTX
 NCBI GI g548605
 BLAST score 232
 E value 1.0e-20
 Match length 64
 % identity 88
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 398435
 Seq. ID LIB3431-014-P1-N1-F5
 Method BLASTN
 NCBI GI g11957
 BLAST score 63
 E value 7.0e-27
 Match length 143
 % identity 43
 NCBI Description Rice complete chloroplast genome

Seq. No. 398436
 Seq. ID LIB3431-014-P1-N1-F6
 Method BLASTX

NCBI GI g1346771
 BLAST score 189
 E value 2.0e-17
 Match length 67
 % identity 78
 NCBI Description PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
 >gi_1086117_pir_S52988 phosphoenolpyruvate carboxykinase
 (PCK1) - Urochloa panicoides >gi_607752 (U09241)
 phosphoenolpyruvate carboxykinase [Urochloa panicoides]

Seq. No. 398437
 Seq. ID LIB3431-014-P1-N1-F9
 Method BLASTX
 NCBI GI g3789954
 BLAST score 277
 E value 2.0e-24
 Match length 54
 % identity 94
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398438
 Seq. ID LIB3431-014-P1-N1-G2
 Method BLASTX
 NCBI GI g2407279
 BLAST score 149
 E value 2.0e-11
 Match length 45
 % identity 81
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 398439
 Seq. ID LIB3431-014-P1-N1-G4
 Method BLASTN
 NCBI GI g20262
 BLAST score 300
 E value 1.0e-168
 Match length 345
 % identity 97
 NCBI Description O.sativa light-induced mRNA

Seq. No. 398440
 Seq. ID LIB3431-014-P1-N1-G6
 Method BLASTN
 NCBI GI g3789949
 BLAST score 142
 E value 2.0e-74
 Match length 146
 % identity 99
 NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No. 398441
 Seq. ID LIB3431-014-P1-N1-G7
 Method BLASTX
 NCBI GI g283039
 BLAST score 157

E value 2.0e-10
 Match length 39
 % identity 79
 NCBI Description gene iojap protein - maize >gi_22349_emb_CAA78772_ (Z15063)
 putative iojap protein [Zea mays]

Seq. No. 398442
 Seq. ID LIB3431-014-P1-N1-H1
 Method BLASTX
 NCBI GI g729478
 BLAST score 247
 E value 1.0e-23
 Match length 60
 % identity 83
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
 reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
 (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
 a region of the predicted gene.; similar to
 ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 398443
 Seq. ID LIB3431-014-P1-N1-H3
 Method BLASTN
 NCBI GI g3075487
 BLAST score 80
 E value 5.0e-37
 Match length 205
 % identity 90
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No. 398444
 Seq. ID LIB3431-014-P1-N1-H8
 Method BLASTX
 NCBI GI g4666287
 BLAST score 336
 E value 1.0e-31
 Match length 65
 % identity 100
 NCBI Description (D85764) cytosolic monodehydroascorbate reductase [Oryza
 sativa]

Seq. No. 398445
 Seq. ID LIB3431-014-P1-N1-H9
 Method BLASTN
 NCBI GI g3075487
 BLAST score 241
 E value 1.0e-133
 Match length 253
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No. 398446
 Seq. ID LIB3431-015-P1-K1-A10
 Method BLASTX

000101 9T04B66

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 398472
Seq. ID LIB3431-015-P1-K1-D5
Method BLASTX
NCBI GI g2196672
BLAST score 444
E value 4.0e-44
Match length 93
% identity 89
NCBI Description (Y08807) HMGd1 [Zea mays]

Seq. No. 398473
Seq. ID LIB3431-015-P1-K1-D7
Method BLASTX
NCBI GI g4455180
BLAST score 184
E value 1.0e-13
Match length 44
% identity 82
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 398474
Seq. ID LIB3431-015-P1-K1-D9
Method BLASTX
NCBI GI g3885888
BLAST score 282
E value 3.0e-25
Match length 63
% identity 90
NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 398475
Seq. ID LIB3431-015-P1-K1-E1
Method BLASTN
NCBI GI g295500
BLAST score 50
E value 4.0e-19
Match length 102
% identity 87
NCBI Description Triticum aestivum heat shock protein 16.9C (hsp16.9C) mRNA, 3' end

Seq. No. 398476
Seq. ID LIB3431-015-P1-K1-E11
Method BLASTN
NCBI GI g6015437
BLAST score 37
E value 3.0e-11
Match length 48
% identity 66
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398477
Seq. ID LIB3431-015-P1-K1-E12
Method BLASTN

[Arabidopsis thaliana]

Seq. No. 398483
 Seq. ID LIB3431-015-P1-K1-F10
 Method BLASTX
 NCBI GI g399213
 BLAST score 501
 E value 6.0e-51
 Match length 119
 % identity 82
 NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG CD4B PRECURSOR >gi_100190_pir_B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum]

Seq. No. 398484
 Seq. ID LIB3431-015-P1-K1-F11
 Method BLASTX
 NCBI GI g3128228
 BLAST score 520
 E value 1.0e-54
 Match length 124
 % identity 88
 NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 398485
 Seq. ID LIB3431-015-P1-K1-F2
 Method BLASTX
 NCBI GI g2497903
 BLAST score 220
 E value 6.0e-18
 Match length 59
 % identity 68
 NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1752831_dbj_BAA14038.1 (D89931) metallothionein-like protein [Oryza sativa] >gi_1815628 (U43530) metallothionein-like type 2 [Oryza sativa]

Seq. No. 398486
 Seq. ID LIB3431-015-P1-K1-F3
 Method BLASTX
 NCBI GI g115787
 BLAST score 578
 E value 6.0e-60
 Match length 112
 % identity 98
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398487
 Seq. ID LIB3431-015-P1-K1-F4
 Method BLASTX

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Seq. No. 398503
 Seq. ID LIB3431-015-P1-K1-H2
 Method BLASTX
 NCBI GI g4455180
 BLAST score 396
 E value 1.0e-38
 Match length 108
 % identity 71
 NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 398504
 Seq. ID LIB3431-015-P1-K1-H3
 Method BLASTX
 NCBI GI g3913811
 BLAST score 704
 E value 1.0e-74
 Match length 141
 % identity 99
 NCBI Description GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
 >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA
 reductase [Oryza sativa]

Seq. No. 398505
 Seq. ID LIB3431-015-P1-K1-H6
 Method BLASTN
 NCBI GI g2072554
 BLAST score 212
 E value 1.0e-116
 Match length 260
 % identity 96
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 398506
 Seq. ID LIB3431-015-P1-K1-H7
 Method BLASTX
 NCBI GI g3075488
 BLAST score 211
 E value 6.0e-17
 Match length 57
 % identity 72
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 398507
 Seq. ID LIB3431-015-P1-K1-H8
 Method BLASTX
 NCBI GI g3915309
 BLAST score 159
 E value 9.0e-11
 Match length 93
 % identity 32
 NCBI Description D-XYLOSE-PROTON SYMPORT (D-XYLOSE TRANSPORTER) >gi_2895856
 (AF045552) D-xylose proton-symporter [Lactobacillus brevis]

Seq. No. 398508
 Seq. ID LIB3431-015-P1-K1-H9

Match length 43
% identity 100
NCBI Description Rice cablR gene for light harvesting chlorophyll
a/b-binding protein

Seq. No. 398540
Seq. ID LIB3431-016-P1-K1-D11
Method BLASTX
NCBI GI g4914457
BLAST score 303
E value 1.0e-27
Match length 105
% identity 52
NCBI Description (AL050400) putative protein [Arabidopsis thaliana]

Seq. No. 398541
Seq. ID LIB3431-016-P1-K1-D12
Method BLASTX
NCBI GI g927025
BLAST score 196
E value 5.0e-15
Match length 116
% identity 38
NCBI Description (L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No. 398542
Seq. ID LIB3431-016-P1-K1-D2
Method BLASTX
NCBI GI g2129950
BLAST score 646
E value 8.0e-68
Match length 132
% identity 98
NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP9) -
common tobacco

Seq. No. 398543
Seq. ID LIB3431-016-P1-K1-D4
Method BLASTX
NCBI GI g115813
BLAST score 423
E value 1.0e-41
Match length 117
% identity 73
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III
chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 398544
Seq. ID LIB3431-016-P1-K1-D6
Method BLASTX
NCBI GI g3789954
BLAST score 743
E value 4.0e-79
Match length 134
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

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Seq. No.      398546
Seq. ID      LIB3431-016-P1-K1-D9
Method       BLASTX
NCBI GI      g2245136
BLAST score   289
E value      6.0e-26
Match length  92
% identity   62
NCBI Description (Z97344) trehalose-6-phosphate synthase like protein
               [Arabidopsis thaliana]
```

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Seq. No.      298548
Seq. ID      LIB3431-016-P1-K1-E11
Method       BLASTX
NCBI GI      g132105
BLAST score   715
E value      7.0e-76
Match length  132
% identity    99
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
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E value 3.0e-11
Match length 57
% identity 91
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No. 398555
Seq. ID LIB3431-016-P1-K1-F10
Method BLASTX
NCBI GI g730456
BLAST score 569
E value 9.0e-59
Match length 108
% identity 99
NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 398556
Seq. ID LIB3431-016-P1-K1-F2
Method BLASTX
NCBI GI g2493318
BLAST score 171
E value 4.0e-12
Match length 72
% identity 46
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_
(Z25471) blue copper protein [Pisum sativum]
>gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No. 398557
Seq. ID LIB3431-016-P1-K1-F5
Method BLASTX
NCBI GI g2072555
BLAST score 232
E value 7.0e-20
Match length 44
% identity 98
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 398558
Seq. ID LIB3431-016-P1-K1-F7
Method BLASTX
NCBI GI g1707998
BLAST score 262
E value 2.0e-23
Match length 52
% identity 98
NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
(SHMT) >gi_481944_pir__S40218 glycine
hydroxymethyltransferase (EC 2.1.2.1) - potato
>gi_438247_emb_CAA81082_ (Z25863) glycine
hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 398559
Seq. ID LIB3431-016-P1-K1-F8
Method BLASTX

NCBI GI g4220481
 BLAST score 205
 E value 4.0e-16
 Match length 107
 % identity 43
 NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 398560
 Seq. ID LIB3431-016-P1-K1-G1
 Method BLASTX
 NCBI GI g115787
 BLAST score 695
 E value 2.0e-73
 Match length 134
 % identity 99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398561
 Seq. ID LIB3431-016-P1-K1-G10
 Method BLASTX
 NCBI GI g4455323
 BLAST score 397
 E value 1.0e-38
 Match length 136
 % identity 59
 NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 398562
 Seq. ID LIB3431-016-P1-K1-G11
 Method BLASTX
 NCBI GI g462195
 BLAST score 423
 E value 1.0e-41
 Match length 88
 % identity 91
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir_S21636 GOS2 protein - rice >gi_20238_emb_CAA36190 (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 398563
 Seq. ID LIB3431-016-P1-K1-G12
 Method BLASTX
 NCBI GI g2501189
 BLAST score 402
 E value 3.0e-39
 Match length 111
 % identity 72
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme

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Seq. No.      398565
Seq. ID      LIB3431-016-P1-K1-G4
Method       BLASTX
NCBI GI      g710308
BLAST score   268
E value      1.0e-23
Match length  49
% identity    96
NCBI Description (U11693) victorin binding protein [Avena sativa]
```

```
Seq. No.      398567
Seq. ID      LIB3431-016-P1-K1-G6
Method       BLASTX
NCBI GI      g3789954
BLAST score   515
E value      2.0e-52
Match length  96
% identity    100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
```

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Seq. No. 398588
 Seq. ID LIB3431-017-P1-K1-A9
 Method BLASTX
 NCBI GI g4337192
 BLAST score 292
 E value 3.0e-26
 Match length 90
 % identity 66
 NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398589
 Seq. ID LIB3431-017-P1-K1-B1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398590
 Seq. ID LIB3431-017-P1-K1-B10
 Method BLASTX
 NCBI GI g733454
 BLAST score 589
 E value 4.0e-61
 Match length 124
 % identity 87
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 398591
 Seq. ID LIB3431-017-P1-K1-B11
 Method BLASTX
 NCBI GI g542200
 BLAST score 263
 E value 7.0e-23
 Match length 98
 % identity 56
 NCBI Description hypothetical protein - garden asparagus
 >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No. 398592
 Seq. ID LIB3431-017-P1-K1-B2
 Method BLASTN
 NCBI GI g21843
 BLAST score 96
 E value 2.0e-46
 Match length 312
 % identity 87
 NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II


```
Method          BLASTX
NCBI GI         g3789952
BLAST score     383
E value         3.0e-37
Match length    85
% identity      98
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
```

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Seq. No.          398638
Seq. ID          LIB3431-017-P1-K1-H11
Method           BLASTX
NCBI GI          g5919219
BLAST score      202
E value          1.0e-15
Match length     133
% identity       13
NCBI Description (AF186273) leucine-rich repeats containing F-box protein
                  FBL3 [Homo sapiens]
```

Seq. No.	398639
Seq. ID	LIB3431-017-P1-K1-H12
Method	BLASTN
NCBI GI	g6015437
BLAST score	33
E value	4.0e-09
Match length	33
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

```
Seq. No.      398640
Seq. ID      LIB3431-017-P1-K1-H2
Method       BLASTX
NCBI GI      g3885892
BLAST score   442
E value      8.0e-44
Match length  85
% identity    98
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
```

```
Seq. No.      398641
Seq. ID      LIB3431-017-P1-K1-H3
Method       BLASTX
NCBI GI      g3075488
BLAST score   426
E value      6.0e-42
Match length  82
% identity   99
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
```

```
Seq. No.      398642
Seq. ID      LIB3431-017-P1-K1-H4
Method       BLASTX
NCBI GI      g1173189
BLAST score   220
E value      8.0e-18
Match length  42
```


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NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 398648
Seq. ID LIB3431-017-P1-N1-A4
Method BLASTN
NCBI GI g2072554
BLAST score 361
E value 0.0e+00
Match length 369
% identity 99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 398649
Seq. ID LIB3431-017-P1-N1-A5
Method BLASTX
NCBI GI g347451
BLAST score 365
E value 6.0e-35
Match length 69
% identity 99
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 398650
Seq. ID LIB3431-017-P1-N1-A7
Method BLASTN
NCBI GI g218209
BLAST score 187
E value 1.0e-101
Match length 235
% identity 95
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 398651
Seq. ID LIB3431-017-P1-N1-A8
Method BLASTN
NCBI GI g886692
BLAST score 377
E value 0.0e+00
Match length 385
% identity 99
NCBI Description O.sativa mRNA for lipid transfer protein, b1

Seq. No. 398652
Seq. ID LIB3431-017-P1-N1-B1
Method BLASTN
NCBI GI g2072554
BLAST score 160
E value 8.0e-85
Match length 244
% identity 91
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

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```
Seq. No.      398654
Seq. ID      LIB3431-017-P1-N1-B2
Method       BLASTX
NCBI GI      g482311
BLAST score   260
E value      1.0e-22
Match length  51
% identity    100
NCBI Description  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
```

```
Seq. No.      398656
Seq. ID      LIB3431-017-P1-N1-B5
Method       BLASTX
NCBI GI      g5541681
BLAST score   182
E value      2.0e-13
Match length  79
% identity    58
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      398657
Seq. ID      LIB3431-017-P1-N1-C1
Method       BLASTX
NCBI GI      g586339
BLAST score   182
E value      2.0e-13
Match length  67
% identity    46
NCBI Description PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir_S46098
probable AMP-binding protein - yeast (Saccharomyces
cerevisiae) >gi_536615_emb_CAA85185_(Z36091) ORF YBR222c
```

09684016 301000

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Seq. No.      398662
Seq. ID       LIB3431-017-P1-N1-C3
Method        BLASTX
NCBI GI       g450231
BLAST score   186
E value       8.0e-14
Match length  56
% identity    59
NCBI Description (U05041) lipoxxygenase [Cuscuta reflexa]
```


Seq. No.	398692
Seq. ID	LIB3431-017-P1-N1-H2
Method	BLASTN
NCBI GI	g3885891
BLAST score	207
E value	1.0e-113
Match length	247
% identity	96
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds
Seq. No.	398693
Seq. ID	LIB3431-017-P1-N1-H3
Method	BLASTX
NCBI GI	g3075488
BLAST score	176
E value	9.0e-13
Match length	33
% identity	100
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.	398694
Seq. ID	LIB3431-017-P1-N1-H4
Method	BLASTN
NCBI GI	g2072554
BLAST score	140
E value	7.0e-73
Match length	248
% identity	88
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds
Seq. No.	398695
Seq. ID	LIB3431-017-P1-N1-H5
Method	BLASTN
NCBI GI	g4105560
BLAST score	141
E value	2.0e-73
Match length	190
% identity	94
NCBI Description	Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA, complete cds
Seq. No.	398696
Seq. ID	LIB3431-017-P1-N1-H7
Method	BLASTX
NCBI GI	g4126473
BLAST score	195
E value	5.0e-15
Match length	47
% identity	81
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]
Seq. No.	398697
Seq. ID	LIB3431-017-P1-N1-H9
Method	BLASTN

Seq. No. 398730
 Seq. ID LIB3431-018-P1-K1-F8
 Method BLASTX
 NCBI GI g2570499
 BLAST score 191
 E value 1.0e-14
 Match length 38
 % identity 100
 NCBI Description (AF022732) 23kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 398731
 Seq. ID LIB3431-018-P1-K1-G10
 Method BLASTX
 NCBI GI g5305740
 BLAST score 759
 E value 8.0e-81
 Match length 186
 % identity 84
 NCBI Description (AF135862) precursor monofunctional aspartokinase [Glycine max]

Seq. No. 398732
 Seq. ID LIB3431-018-P1-K1-G11
 Method BLASTX
 NCBI GI g115787
 BLAST score 691
 E value 7.0e-73
 Match length 133
 % identity 99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398733
 Seq. ID LIB3431-018-P1-K1-G12
 Method BLASTX
 NCBI GI g5921185
 BLAST score 395
 E value 6.0e-47
 Match length 213
 % identity 50
 NCBI Description CYTOCHROME P450 76C1 >gi_2979548 (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No. 398734
 Seq. ID LIB3431-018-P1-K1-G2
 Method BLASTX
 NCBI GI g1173347
 BLAST score 932
 E value 1.0e-101
 Match length 185
 % identity 95
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)

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Seq. No.      398736
Seq. ID      LIB3431-018-P1-K1-G5
Method       BLASTX
NCBI GI      g6014904
BLAST score   296
E value      1.0e-26
Match length  74
% identity    77
NCBI Description  DAG PROTEIN, CHLOROPLAST PRECURSOR
                >gi 1200205 emb CAA65064 (X95753) DAG [Antirrhinum majus]
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Seq. No.          398737
Seq. ID           LIB3431-018-P1-K1-G6
Method            BLASTX
NCBI GI           g2501189
BLAST score       643
E value           3.0e-67
Match length      164
% identity        79
NCBI Description   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
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Seq. No.	398739
Seq. ID	LIB3431-018-P1-K1-G9
Method	BLASTX
NCBI GI	g3885888
BLAST score	326
E value	4.0e-30
Match length	89
% identity	76
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]
Seq. No.	398740
Seq. ID	LIB3431-018-P1-K1-H10
Method	BLASTX
NCBI GI	g115793
BLAST score	869
E value	1.0e-93
Match length	192
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]
Seq. No.	398741
Seq. ID	LIB3431-018-P1-K1-H12
Method	BLASTX
NCBI GI	g710308
BLAST score	987
E value	1.0e-107
Match length	224
% identity	85
NCBI Description	(U11693) victorin binding protein [Avena sativa]
Seq. No.	398742
Seq. ID	LIB3431-018-P1-K1-H3
Method	BLASTX
NCBI GI	g113466
BLAST score	282
E value	8.0e-25
Match length	82
% identity	65
NCBI Description	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_72020_pir_XWNC ADP,ATP carrier protein - Neurospora crassa >gi_2977_emb_CAA25104_ (X00363) ADP/ATP carrier protein [Neurospora crassa]
Seq. No.	398743
Seq. ID	LIB3431-018-P1-K1-H4
Method	BLASTX
NCBI GI	g3126854
BLAST score	731
E value	2.0e-77
Match length	186
% identity	80
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398744
 Seq. ID LIB3431-018-P1-K1-H5
 Method BLASTX
 NCBI GI g121530
 BLAST score 866
 E value 3.0e-93
 Match length 194
 % identity 86
 NCBI Description (S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL (GLYCOLATE OXIDASE) (GOX) (SHORT CHAIN ALPHA-HYDROXY ACID OXIDASE)
 >gi_65974_pir_OXSPH (S)-2-hydroxy-acid oxidase (EC 1.1.3.15), peroxisomal - spinach >gi_229945_pdb_1GOX Glycolate Oxidase (E.C.1.1.3.1) >gi_170113 (J03492) glycolate oxidase (EC 1.1.3.15) [Spinacia oleracea]

Seq. No. 398745
 Seq. ID LIB3431-018-P1-K1-H7
 Method BLASTX
 NCBI GI g3345477
 BLAST score 813
 E value 4.0e-87
 Match length 201
 % identity 79
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398746
 Seq. ID LIB3431-018-P1-N1-A1
 Method BLASTX
 NCBI GI g70772
 BLAST score 292
 E value 2.0e-26
 Match length 58
 % identity 100
 NCBI Description histone H4 - wheat >gi_70773_pir_HSPM4 histone H4 - garden pea

Seq. No. 398747
 Seq. ID LIB3431-018-P1-N1-A2
 Method BLASTX
 NCBI GI g3789954
 BLAST score 390
 E value 1.0e-37
 Match length 72
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398748
 Seq. ID LIB3431-018-P1-N1-A4
 Method BLASTX
 NCBI GI g4038034
 BLAST score 222
 E value 4.0e-19
 Match length 76
 % identity 68
 NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 398749
 Seq. ID LIB3431-018-P1-N1-A6
 Method BLASTX
 NCBI GI g132166
 BLAST score 158
 E value 1.0e-10
 Match length 31
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
 activase precursor - Arabidopsis thaliana
 >gi_16471_emb_CAA32429 (X14212) rubisco activase (AA 1 -
 473) [Arabidopsis thaliana]

Seq. No. 398750
 Seq. ID LIB3431-018-P1-N1-A7
 Method BLASTX
 NCBI GI g4836912
 BLAST score 238
 E value 5.0e-20
 Match length 73
 % identity 66
 NCBI Description (AC007153) 60811 [Arabidopsis thaliana]

Seq. No. 398751
 Seq. ID LIB3431-018-P1-N1-A8
 Method BLASTX
 NCBI GI g2326947
 BLAST score 158
 E value 1.0e-10
 Match length 29
 % identity 100
 NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor
 [Zea mays]

Seq. No. 398752
 Seq. ID LIB3431-018-P1-N1-A9
 Method BLASTN
 NCBI GI g2570514
 BLAST score 259
 E value 1.0e-143
 Match length 332
 % identity 97
 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 398753
 Seq. ID LIB3431-018-P1-N1-B3
 Method BLASTX
 NCBI GI g1172818
 BLAST score 179
 E value 2.0e-25
 Match length 67
 % identity 97
 NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal
 protein S16 [Oryza sativa] >gi_1096552_prf_2111468A

0963401 III 1000000

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Seq. No.          398755
Seq. ID           LIB3431-018-P1-N1-B6
Method            BLASTX
NCBI GI           g115813
BLAST score       224
E value           3.0e-18
Match length      78
% identity        69
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
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Seq. No.	398757
Seq. ID	LIB3431-018-P1-N1-B9
Method	BLASTN
NCBI GI	g11957
BLAST score	68
E value	4.0e-30
Match length	156
% identity	87
NCBI Description	Rice complete chloroplast genome

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Seq. No. 398759
 Seq. ID LIB3431-018-P1-N1-C4
 Method BLASTX
 NCBI GI g671740
 BLAST score 244
 E value 8.0e-21
 Match length 58
 % identity 79
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 398760
 Seq. ID LIB3431-018-P1-N1-C5
 Method BLASTX
 NCBI GI g548605
 BLAST score 338
 E value 9.0e-32
 Match length 73
 % identity 92
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 398761
 Seq. ID LIB3431-018-P1-N1-C6
 Method BLASTX
 NCBI GI g2407273
 BLAST score 268
 E value 1.0e-23
 Match length 53
 % identity 96
 NCBI Description (AF017359) lipid transfer protein LPT II [Oryza sativa]

Seq. No. 398762
 Seq. ID LIB3431-018-P1-N1-C8
 Method BLASTX
 NCBI GI g3980406
 BLAST score 313
 E value 8.0e-29
 Match length 93
 % identity 61
 NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No. 398763
 Seq. ID LIB3431-018-P1-N1-D12
 Method BLASTX
 NCBI GI g115813
 BLAST score 267
 E value 3.0e-23
 Match length 83
 % identity 69
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

NCBI Description O.sativa mRNA for catalase

Seq. No. 398769
 Seq. ID LIB3431-018-P1-N1-E1
 Method BLASTX
 NCBI GI g3913641
 BLAST score 434
 E value 1.0e-60
 Match length 126
 % identity 96
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_3041777_dbj_BAA25423_ (AB007194)
 fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 398770
 Seq. ID LIB3431-018-P1-N1-E10
 Method BLASTN
 NCBI GI g21838
 BLAST score 67
 E value 3.0e-29
 Match length 204
 % identity 85
 NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase

Seq. No. 398771
 Seq. ID LIB3431-018-P1-N1-E11
 Method BLASTX
 NCBI GI g2864617
 BLAST score 200
 E value 2.0e-15
 Match length 85
 % identity 53
 NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like
 protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1_
 (AJ245574) ATP synthase beta chain precursor (subunit II)
 [Arabidopsis thaliana]

Seq. No. 398772
 Seq. ID LIB3431-018-P1-N1-E12
 Method BLASTX
 NCBI GI g671740
 BLAST score 284
 E value 3.0e-25
 Match length 63
 % identity 84
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 398773
 Seq. ID LIB3431-018-P1-N1-E2
 Method BLASTX
 NCBI GI g2407279
 BLAST score 279
 E value 4.0e-42
 Match length 94
 % identity 93

000101-97048960

NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 398774
 Seq. ID LIB3431-018-P1-N1-E3
 Method BLASTN
 NCBI GI g2072554
 BLAST score 455
 E value 0.0e+00
 Match length 483
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 398775
 Seq. ID LIB3431-018-P1-N1-E5
 Method BLASTX
 NCBI GI g2582822
 BLAST score 285
 E value 3.0e-34
 Match length 90
 % identity 82
 NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No. 398776
 Seq. ID LIB3431-018-P1-N1-E7
 Method BLASTN
 NCBI GI g2331130
 BLAST score 162
 E value 6.0e-86
 Match length 254
 % identity 91
 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No. 398777
 Seq. ID LIB3431-018-P1-N1-E9
 Method BLASTX
 NCBI GI g3036951
 BLAST score 291
 E value 3.0e-26
 Match length 56
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]

Seq. No. 398778
 Seq. ID LIB3431-018-P1-N1-F1
 Method BLASTN
 NCBI GI g2072554
 BLAST score 140
 E value 7.0e-73
 Match length 272
 % identity 88
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	398779
Seq. ID	LIB3431-018-P1-N1-F10
Method	BLASTX
NCBI GI	g548605
BLAST score	368
E value	3.0e-35
Match length	76
% identity	95
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]
Seq. No.	398780
Seq. ID	LIB3431-018-P1-N1-F11
Method	BLASTX
NCBI GI	g482311
BLAST score	297
E value	3.0e-41
Match length	91
% identity	99
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	398781
Seq. ID	LIB3431-018-P1-N1-F5
Method	BLASTN
NCBI GI	g20369
BLAST score	382
E value	0.0e+00
Match length	382
% identity	100
NCBI Description	Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31) >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase
Seq. No.	398782
Seq. ID	LIB3431-018-P1-N1-F7
Method	BLASTX
NCBI GI	g1477428
BLAST score	294
E value	2.0e-26
Match length	59
% identity	97
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]
Seq. No.	398783
Seq. ID	LIB3431-018-P1-N1-F8
Method	BLASTX
NCBI GI	g4079798
BLAST score	298
E value	8.0e-43
Match length	93
% identity	88

Seq. No. 398789
 Seq. ID LIB3431-018-P1-N1-G9
 Method BLASTN
 NCBI GI g3885887
 BLAST score 365
 E value 0.0e+00
 Match length 365
 % identity 100
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 398790
 Seq. ID LIB3431-018-P1-N1-H10
 Method BLASTX
 NCBI GI g115794
 BLAST score 542
 E value 2.0e-55
 Match length 114
 % identity 90
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_(X60275) LHCII type III [Lycopersicon esculentum]

Seq. No. 398791
 Seq. ID LIB3431-018-P1-N1-H12
 Method BLASTN
 NCBI GI g710307
 BLAST score 36
 E value 1.0e-10
 Match length 52
 % identity 92
 NCBI Description Avena sativa victorin binding protein mRNA, complete cds

Seq. No. 398792
 Seq. ID LIB3431-018-P1-N1-H2
 Method BLASTX
 NCBI GI g3881189
 BLAST score 146
 E value 2.0e-15
 Match length 93
 % identity 43
 NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y

Seq. No. 398793
 Seq. ID LIB3431-018-P1-N1-H4
 Method BLASTX
 NCBI GI g115802
 BLAST score 195
 E value 5.0e-15
 Match length 40
 % identity 90

Match length	137
% identity	57
NCBI Description	(AF159254) ascorbate peroxidase [<i>Zantedeschia aethiopica</i>]
Seq. No.	398804
Seq. ID	LIB3431-019-P1-K1-A7
Method	BLASTX
NCBI GI	g320618
BLAST score	689
E value	9.0e-73
Match length	150
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [<i>Oryza sativa</i>] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [<i>Oryza sativa</i>]
Seq. No.	398805
Seq. ID	LIB3431-019-P1-K1-A9
Method	BLASTX
NCBI GI	g2982453
BLAST score	149
E value	9.0e-15
Match length	77
% identity	58
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [<i>Arabidopsis thaliana</i>]
Seq. No.	398806
Seq. ID	LIB3431-019-P1-K1-B1
Method	BLASTX
NCBI GI	g2809245
BLAST score	298
E value	6.0e-27
Match length	78
% identity	72
NCBI Description	(AC002560) F21B7.14 [<i>Arabidopsis thaliana</i>]
Seq. No.	398807
Seq. ID	LIB3431-019-P1-K1-B11
Method	BLASTX
NCBI GI	g4038594
BLAST score	280
E value	8.0e-25
Match length	84
% identity	62
NCBI Description	(AJ222798) tDET1 protein [<i>Lycopersicon esculentum</i>] >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [<i>Lycopersicon esculentum</i>]
Seq. No.	398808
Seq. ID	LIB3431-019-P1-K1-B12
Method	BLASTX
NCBI GI	g3885882
BLAST score	390
E value	7.0e-38

Match length 74
 % identity 100
 NCBI Description (AF093629) inorganic pyrophosphatase [*Oryza sativa*]

 Seq. No. 398809
 Seq. ID LIB3431-019-P1-K1-B4
 Method BLASTX
 NCBI GI g4585882
 BLAST score 590
 E value 3.0e-61
 Match length 134
 % identity 78
 NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein [*Arabidopsis thaliana*]

Seq. No. 398810
 Seq. ID LIB3431-019-P1-K1-B6
 Method BLASTX
 NCBI GI g2921158
 BLAST score 554
 E value 4.0e-57
 Match length 122
 % identity 89
 NCBI Description (AF022909) ClpC [*Arabidopsis thaliana*]

Seq. No. 398811
 Seq. ID LIB3431-019-P1-K1-B7
 Method BLASTX
 NCBI GI g320618
 BLAST score 753
 E value 3.0e-80
 Match length 142
 % identity 99
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [*Oryza sativa*]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [*Oryza sativa*]

Seq. No. 398812
 Seq. ID LIB3431-019-P1-K1-B8
 Method BLASTX
 NCBI GI g132105
 BLAST score 427
 E value 3.0e-42
 Match length 103
 % identity 83
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [*Oryza sativa*] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza*
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [*Oryza sativa*]

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Seq. No.          398824
Seq. ID          LIB3431-019-P1-K1-D10
Method           BLASTX
NCBI GI          g1835731
BLAST score      512
E value          4.0e-52
Match length     97
% identity       100
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

Seq. No.	398826
Seq. ID	LIB3431-019-P1-K1-D12
Method	BLASTX
NCBI GI	g671740
BLAST score	588
E value	5.0e-61
Match length	108
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

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E value 5.0e-66
 Match length 139
 % identity 91
 NCBI Description UROPORPHYRINOGEN DECARBOXYLASE (UPD)
 >gi_1362169_pir_S55733 uroporphyrinogen decarboxylase -
 barley >gi_1016347_emb_CAA58039_ (X82832) uroporphyrinogen
 decarboxylase [Hordeum vulgare]

Seq. No. 398828
 Seq. ID LIB3431-019-P1-K1-D4
 Method BLASTN
 NCBI GI g6015437
 BLAST score 38
 E value 7.0e-12
 Match length 38
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398829
 Seq. ID LIB3431-019-P1-K1-D5
 Method BLASTN
 NCBI GI g3821780
 BLAST score 36
 E value 1.0e-10
 Match length 47
 % identity 66
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 398830
 Seq. ID LIB3431-019-P1-K1-D7
 Method BLASTX
 NCBI GI g115787
 BLAST score 508
 E value 1.0e-51
 Match length 117
 % identity 87
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 398831
 Seq. ID LIB3431-019-P1-K1-D8
 Method BLASTX
 NCBI GI g132105
 BLAST score 609
 E value 2.0e-63
 Match length 131
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

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Seq. No.          398846
Seq. ID          LIB3431-019-P1-K1-F4
Method           BLASTX
NCBI GI          g82080
BLAST score      336
E value          2.0e-31
Match length     95
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E value 3.0e-42
 Match length 95
 % identity 95
 NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No. 398862
 Seq. ID LIB3431-019-P1-K1-H6
 Method BLASTX
 NCBI GI g2795806
 BLAST score 498
 E value 2.0e-50
 Match length 141
 % identity 70
 NCBI Description (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No. 398863
 Seq. ID LIB3431-019-P1-K1-H7
 Method BLASTX
 NCBI GI g1164988
 BLAST score 345
 E value 2.0e-32
 Match length 124
 % identity 55
 NCBI Description (X94335) YOR3513c [Saccharomyces cerevisiae]

Seq. No. 398864
 Seq. ID LIB3431-019-P1-K1-H9
 Method BLASTX
 NCBI GI g266893
 BLAST score 661
 E value 1.0e-69
 Match length 130
 % identity 95
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_322416_pir_S28172 ribulose-bisphosphate carboxylase
 activase - cucumber >gi_18284_emb_CAA47906_ (X67674)
 rubisco activase [Cucumis sativus]

Seq. No. 398865
 Seq. ID LIB3431-019-P1-N1-A10
 Method BLASTN
 NCBI GI g2072554
 BLAST score 233
 E value 1.0e-128
 Match length 237
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 398866
 Seq. ID LIB3431-019-P1-N1-A11
 Method BLASTX
 NCBI GI g1085987
 BLAST score 231
 E value 2.0e-19
 Match length 45

% identity 98
 NCBI Description light harvesting chlorophyll a protein precursor - Norway spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]

Seq. No. 398867
 Seq. ID LIB3431-019-P1-N1-A2
 Method BLASTN
 NCBI GI g218207
 BLAST score 161
 E value 2.0e-85
 Match length 245
 % identity 91
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 398868
 Seq. ID LIB3431-019-P1-N1-A4
 Method BLASTX
 NCBI GI g3789954
 BLAST score 390
 E value 1.0e-37
 Match length 72
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398869
 Seq. ID LIB3431-019-P1-N1-A6
 Method BLASTX
 NCBI GI g5442410
 BLAST score 179
 E value 5.0e-13
 Match length 78
 % identity 49
 NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 398870
 Seq. ID LIB3431-019-P1-N1-A7
 Method BLASTX
 NCBI GI g115787
 BLAST score 409
 E value 6.0e-40
 Match length 77
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398871
 Seq. ID LIB3431-019-P1-N1-A9
 Method BLASTX
 NCBI GI g2191138
 BLAST score 287

E value 1.0e-25
 Match length 64
 % identity 83
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No. 398872
 Seq. ID LIB3431-019-P1-N1-B1
 Method BLASTX
 NCBI GI g2809245
 BLAST score 283
 E value 3.0e-25
 Match length 64
 % identity 83
 NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No. 398873
 Seq. ID LIB3431-019-P1-N1-B11
 Method BLASTX
 NCBI GI g4038594
 BLAST score 233
 E value 2.0e-19
 Match length 67
 % identity 63
 NCBI Description (AJ222798) tDET1 protein [Lycopersicon esculentum]
 >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]

Seq. No. 398874
 Seq. ID LIB3431-019-P1-N1-B12
 Method BLASTN
 NCBI GI g3885881
 BLAST score 345
 E value 0.0e+00
 Match length 373
 % identity 98
 NCBI Description Oryza sativa inorganic pyrophosphatase (IPP) mRNA, complete cds

Seq. No. 398875
 Seq. ID LIB3431-019-P1-N1-B4
 Method BLASTX
 NCBI GI g115813
 BLAST score 176
 E value 1.0e-12
 Match length 41
 % identity 80
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 398876
 Seq. ID LIB3431-019-P1-N1-B6
 Method BLASTX
 NCBI GI g461753
 BLAST score 406
 E value 1.0e-39

Match length 103
 % identity 77
 NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
 PRECURSOR >gi_419773_pir_S31164 ATP-dependent ClpB
 proteinase regulatory chain homolog precursor, chloroplast
 - garden pea >gi_169128 (L09547) nuclear encoded precursor
 to chloroplast protein [Pisum sativum]

Seq. No. 398877
 Seq. ID LIB3431-019-P1-N1-B7
 Method BLASTN
 NCBI GI g20181
 BLAST score 139
 E value 3.0e-72
 Match length 150
 % identity 98
 NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 398878
 Seq. ID LIB3431-019-P1-N1-B8
 Method BLASTX
 NCBI GI g671740
 BLAST score 363
 E value 2.0e-34
 Match length 72
 % identity 94
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 398879
 Seq. ID LIB3431-019-P1-N1-C11
 Method BLASTX
 NCBI GI g5031281
 BLAST score 237
 E value 9.0e-20
 Match length 51
 % identity 80
 NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 398880
 Seq. ID LIB3431-019-P1-N1-C3
 Method BLASTN
 NCBI GI g2072554
 BLAST score 282
 E value 1.0e-157
 Match length 286
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 398881
 Seq. ID LIB3431-019-P1-N1-C4
 Method BLASTN
 NCBI GI g218154
 BLAST score 50
 E value 4.0e-19

Match length	78
% identity	91
NCBI Description	Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp
Seq. No.	398882
Seq. ID	LIB3431-019-P1-N1-C5
Method	BLASTX
NCBI GI	g3776005
BLAST score	162
E value	6.0e-11
Match length	36
% identity	89
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.	398883
Seq. ID	LIB3431-019-P1-N1-C7
Method	BLASTN
NCBI GI	g14264
BLAST score	51
E value	1.0e-19
Match length	87
% identity	90
NCBI Description	T.aestivum gene for sedoheptulose-1,7-bisphosphatase
Seq. No.	398884
Seq. ID	LIB3431-019-P1-N1-C8
Method	BLASTN
NCBI GI	g218207
BLAST score	163
E value	1.0e-86
Match length	279
% identity	90
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone POSSS1139
Seq. No.	398885
Seq. ID	LIB3431-019-P1-N1-D10
Method	BLASTX
NCBI GI	g1835731
BLAST score	280
E value	6.0e-25
Match length	64
% identity	84
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.	398886
Seq. ID	LIB3431-019-P1-N1-D11
Method	BLASTX
NCBI GI	g517500
BLAST score	176
E value	8.0e-13
Match length	53
% identity	68
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II

OE17 protein [Pisum sativum]

Seq. No. 398887
 Seq. ID LIB3431-019-P1-N1-D3
 Method BLASTX
 NCBI GI g6014938
 BLAST score 173
 E value 2.0e-12
 Match length 34
 % identity 94
 NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi_3420233
 (AF058763) uroporphyrinogen decarboxylase [Zea mays]

Seq. No. 398888
 Seq. ID LIB3431-019-P1-N1-D7
 Method BLASTX
 NCBI GI g421916
 BLAST score 162
 E value 4.0e-11
 Match length 29
 % identity 100
 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
 >gi_12582_emb_CAA48410_(X68333) light harvesting
 chlorophyll a /b binding protein [Hedera helix]

Seq. No. 398889
 Seq. ID LIB3431-019-P1-N1-D8
 Method BLASTX
 NCBI GI g347451
 BLAST score 387
 E value 2.0e-37
 Match length 72
 % identity 97
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
 sativa].

Seq. No. 398890
 Seq. ID LIB3431-019-P1-N1-D9
 Method BLASTX
 NCBI GI g3036951
 BLAST score 310
 E value 2.0e-28
 Match length 61
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [Nicotiana sylvestris]

Seq. No. 398891
 Seq. ID LIB3431-019-P1-N1-E4
 Method BLASTX
 NCBI GI g5764049
 BLAST score 252
 E value 2.0e-21
 Match length 67
 % identity 70
 NCBI Description (Y16832) alpha-1,3-mannosyl-glycoprotein
 beta-1,2-N-acetylglucosaminyltransferase [Nicotiana

tabacum]

Seq. No. 398892
 Seq. ID LIB3431-019-P1-N1-E6
 Method BLASTN
 NCBI GI g2331130
 BLAST score 189
 E value 1.0e-102
 Match length 193
 % identity 99
 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No. 398893
 Seq. ID LIB3431-019-P1-N1-F10
 Method BLASTN
 NCBI GI g3075487
 BLAST score 240
 E value 1.0e-132
 Match length 260
 % identity 98
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 398894
 Seq. ID LIB3431-019-P1-N1-F2
 Method BLASTX
 NCBI GI g1777961
 BLAST score 194
 E value 1.0e-14
 Match length 73
 % identity 58
 NCBI Description (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No. 398895
 Seq. ID LIB3431-019-P1-N1-F4
 Method BLASTX
 NCBI GI g115813
 BLAST score 243
 E value 1.0e-20
 Match length 55
 % identity 85
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 398896
 Seq. ID LIB3431-019-P1-N1-F6
 Method BLASTX
 NCBI GI g710308
 BLAST score 147
 E value 2.0e-09
 Match length 27
 % identity 96
 NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 398897
 Seq. ID LIB3431-019-P1-N1-F7
 Method BLASTX
 NCBI GI g3126854
 BLAST score 345
 E value 1.0e-32
 Match length 65
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398898
 Seq. ID LIB3431-019-P1-N1-F8
 Method BLASTN
 NCBI GI g1835730
 BLAST score 219
 E value 1.0e-120
 Match length 255
 % identity 96
 NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 398899
 Seq. ID LIB3431-019-P1-N1-F9
 Method BLASTN
 NCBI GI g3075487
 BLAST score 338
 E value 0.0e+00
 Match length 338
 % identity 100
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 398900
 Seq. ID LIB3431-019-P1-N1-G1
 Method BLASTX
 NCBI GI g1321627
 BLAST score 231
 E value 3.0e-19
 Match length 55
 % identity 82
 NCBI Description (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita sp.]

Seq. No. 398901
 Seq. ID LIB3431-019-P1-N1-G10
 Method BLASTX
 NCBI GI g289920
 BLAST score 286
 E value 1.0e-25
 Match length 58
 % identity 95
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 398902
 Seq. ID LIB3431-019-P1-N1-G2
 Method BLASTX

NCBI GI g120661
 BLAST score 251
 E value 2.0e-21
 Match length 50
 % identity 92
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
 PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
 dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 398903
 Seq. ID LIB3431-019-P1-N1-G5
 Method BLASTN
 NCBI GI g218171
 BLAST score 215
 E value 1.0e-117
 Match length 243
 % identity 97
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
 a/b binding protein of photosystem II (LHCPII), complete
 cds

Seq. No. 398904
 Seq. ID LIB3431-019-P1-N1-G6
 Method BLASTX
 NCBI GI g1652203
 BLAST score 153
 E value 5.0e-10
 Match length 78
 % identity 38
 NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 398905
 Seq. ID LIB3431-019-P1-N1-G7
 Method BLASTX
 NCBI GI g132105
 BLAST score 310
 E value 1.0e-30
 Match length 68
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398906
 Seq. ID LIB3431-019-P1-N1-H11
 Method BLASTX
 NCBI GI g3789954
 BLAST score 184
 E value 9.0e-14
 Match length 33
 % identity 97

063416

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Seq. No.      398913
Seq. ID      LIB3431-020-P1-K1-A12
Method       BLASTX
NCBI GI      g115787
BLAST score   516
E value      2.0e-52
Match length  120
% identity    86
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
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Seq. No.      398915
Seq. ID      LIB3431-020-P1-K1-A8
Method       BLASTX
NCBI GI      g3550982
BLAST score   156
E value      2.0e-10
Match length  82
% identity    48
NCBI Description (AB010690) mutM homologue-1 [Arabidopsis thaliana]
>gi.5903053_gb_AAD55612.1_AC008016.22 (AC008016) Identical
to gb_AB010690 mutM homologue-1 (formamidopyrimidine-DNA
glycosylase 1) from Arabidopsis thaliana. EST gb_Z18192
comes from this gene
```

50970

Match length 90
 % identity 58
 NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]

Seq. No. 398922
 Seq. ID LIB3431-020-P1-K1-B9
 Method BLASTX
 NCBI GI g132105
 BLAST score 391
 E value 7.0e-38
 Match length 124
 % identity 64
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398923
 Seq. ID LIB3431-020-P1-K1-C1
 Method BLASTX
 NCBI GI g170404
 BLAST score 565
 E value 3.0e-68
 Match length 137
 % identity 96
 NCBI Description (M14444) chlorophyll a/b-binding protein Cab-3C [Lycopersicon esculentum]

Seq. No. 398924
 Seq. ID LIB3431-020-P1-K1-C10
 Method BLASTX
 NCBI GI g1346874
 BLAST score 152
 E value 8.0e-10
 Match length 49
 % identity 61
 NCBI Description PHOTOSYSTEM II REACTION CENTER W PROTEIN >gi_1016177 (U30821) subunit of the water oxidation complex on the luminal surface of the photosystem II reaction center complex [Cyanophora paradoxa]

Seq. No. 398925
 Seq. ID LIB3431-020-P1-K1-C11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 646
 E value 1.0e-67
 Match length 140
 % identity 89
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398926

Seq. ID	LIB3431-020-P1-K1-C2
Method	BLASTX
NCBI GI	g473878
BLAST score	168
E value	3.0e-12
Match length	46
% identity	70
NCBI Description	(U08315) calnexin homolog [Arabidopsis thaliana]
Seq. No.	398927
Seq. ID	LIB3431-020-P1-K1-C3
Method	BLASTX
NCBI GI	g5729754
BLAST score	175
E value	1.0e-12
Match length	77
% identity	49
NCBI Description	transcription factor CA150 >gi_2460124 (AF017789) putative transcription factor CA150 [Homo sapiens]
Seq. No.	398928
Seq. ID	LIB3431-020-P1-K1-C5
Method	BLASTX
NCBI GI	g500734
BLAST score	374
E value	7.0e-36
Match length	131
% identity	54
NCBI Description	(U10414) Contains similarity to Pfam domain: PF00005 (ABC_tran), Score=245.2, E-value=3e-70, N=2 [Caenorhabditis elegans]
Seq. No.	398929
Seq. ID	LIB3431-020-P1-K1-C7
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	398930
Seq. ID	LIB3431-020-P1-K1-C8
Method	BLASTX
NCBI GI	g1519251
BLAST score	537
E value	4.0e-55
Match length	108
% identity	100
NCBI Description	(U65957) GF14-c protein [Oryza sativa]
Seq. No.	398931
Seq. ID	LIB3431-020-P1-K1-D10
Method	BLASTX

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NCBI GI      g3915131
BLAST score   582
E value      3.0e-60
Match length 112
% identity   100
NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
>gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin
h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza
sativa]

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Seq. No.      398932
Seq. ID      LIB3431-020-P1-K1-D4
Method       BLASTX
NCBI GI      g2570511
BLAST score   662
E value      1.0e-69
Match length  127
% identity    98
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
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Seq. No.      398933
Seq. ID      LIB3431-020-P1-K1-D5
Method       BLASTX
NCBI GI      g3047117
BLAST score   740
E value      1.0e-78
Match length  144
% identity    97
NCBI Description (AF058919) similar to ATP-dependent RNA helicases
               [Arabidopsis thaliana]
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Seq. No.          398934
Seq. ID           LIB3431-020-P1-K1-D7
Method            BLASTX
NCBI GI           g1617206
BLAST score       180
E value           3.0e-13
Match length      49
% identity        71
NCBI Description   (Z72489) CP12 [Pisum sativum]
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Seq. No.      398935
Seq. ID      LIB3431-020-P1-K1-D8
Method       BLASTX
NCBI GI      g320618
BLAST score   632
E value      5.0e-66
Match length  137
% identity    88
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]
```

Seq. No. 398936

Seq. ID LIB3431-020-P1-K1-D9
 Method BLASTX
 NCBI GI g2582822
 BLAST score 458
 E value 1.0e-45
 Match length 108
 % identity 80
 NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No. 398937
 Seq. ID LIB3431-020-P1-K1-E1
 Method BLASTX
 NCBI GI g4886307
 BLAST score 543
 E value 1.0e-55
 Match length 123
 % identity 87
 NCBI Description (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

Seq. No. 398938
 Seq. ID LIB3431-020-P1-K1-E10
 Method BLASTX
 NCBI GI g2570515
 BLAST score 219
 E value 1.0e-17
 Match length 47
 % identity 91
 NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 398939
 Seq. ID LIB3431-020-P1-K1-E11
 Method BLASTX
 NCBI GI g320618
 BLAST score 607
 E value 4.0e-63
 Match length 133
 % identity 87
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 398940
 Seq. ID LIB3431-020-P1-K1-E12
 Method BLASTX
 NCBI GI g132105
 BLAST score 759
 E value 6.0e-81
 Match length 139
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398941
 Seq. ID LIB3431-020-P1-K1-E2
 Method BLASTX
 NCBI GI g3345477
 BLAST score 491
 E value 2.0e-49
 Match length 140
 % identity 69
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398942
 Seq. ID LIB3431-020-P1-K1-E3
 Method BLASTN
 NCBI GI g6015437
 BLAST score 35
 E value 6.0e-10
 Match length 35
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398943
 Seq. ID LIB3431-020-P1-K1-E5
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 398944
 Seq. ID LIB3431-020-P1-K1-E6
 Method BLASTX
 NCBI GI g115787
 BLAST score 417
 E value 7.0e-41
 Match length 121
 % identity 74
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 398945
 Seq. ID LIB3431-020-P1-K1-E7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 559

00684016-101000

E value 2.0e-57
Match length 106
% identity 100
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 398946
Seq. ID LIB3431-020-P1-K1-E8
Method BLASTX
NCBI GI g2407281
BLAST score 625
E value 3.0e-65
Match length 117
% identity 99
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 398947
Seq. ID LIB3431-020-P1-K1-E9
Method BLASTX
NCBI GI g2565305
BLAST score 605
E value 5.0e-63
Match length 119
% identity 96
NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No. 398948
Seq. ID LIB3431-020-P1-K1-F1
Method BLASTN
NCBI GI g3789951
BLAST score 188
E value 1.0e-101
Match length 380
% identity 96
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 398949
Seq. ID LIB3431-020-P1-K1-F11
Method BLASTX
NCBI GI g1661160
BLAST score 523
E value 3.0e-53
Match length 115
% identity 85
NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398950
Seq. ID LIB3431-020-P1-K1-F12
Method BLASTX
NCBI GI g728744
BLAST score 338
E value 1.0e-54
Match length 152
% identity 76

NCBI Description AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390
auxin-induced protein - common tobacco
>gi_19799_emb_CAA39708_ (X56267) auxin-induced protein
[Nicotiana tabacum]

Seq. No. 398951
Seq. ID LIB3431-020-P1-K1-F2
Method BLASTX
NCBI GI g3789952
BLAST score 788
E value 2.0e-84
Match length 152
% identity 96
NCBI Description (AF094775) chlorophyll a/b-binding protein precursor [Oryza
sativa]

Seq. No. 398952
Seq. ID LIB3431-020-P1-K1-F3
Method BLASTX
NCBI GI g115772
BLAST score 211
E value 2.0e-17
Match length 57
% identity 77
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
protein 1R precursor - rice >gi_20178_emb_CAA32108
(X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
[Oryza sativa]

Seq. No. 398953
Seq. ID LIB3431-020-P1-K1-F4
Method BLASTX
NCBI GI g6002055
BLAST score 634
E value 3.0e-66
Match length 151
% identity 77
NCBI Description (AJ249794) lipoxygenase [Arabidopsis thaliana]

Seq. No. 398954
Seq. ID LIB3431-020-P1-K1-F8
Method BLASTX
NCBI GI g3345477
BLAST score 316
E value 5.0e-29
Match length 59
% identity 100
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398955
Seq. ID LIB3431-020-P1-K1-F9
Method BLASTX
NCBI GI g131225
BLAST score 570
E value 7.0e-59
Match length 119

% identity 93
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 398956
 Seq. ID LIB3431-020-P1-K1-G10
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398957
 Seq. ID LIB3431-020-P1-K1-G11
 Method BLASTX
 NCBI GI g2462763
 BLAST score 322
 E value 2.0e-44
 Match length 124
 % identity 79
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 398958
 Seq. ID LIB3431-020-P1-K1-G12
 Method BLASTX
 NCBI GI g871931
 BLAST score 490
 E value 2.0e-49
 Match length 125
 % identity 80
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 398959
 Seq. ID LIB3431-020-P1-K1-G6
 Method BLASTN
 NCBI GI g5670155
 BLAST score 43
 E value 4.0e-15
 Match length 75
 % identity 89
 NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete sequence

Seq. No. 398960
 Seq. ID LIB3431-020-P1-K1-G7
 Method BLASTN
 NCBI GI g21810
 BLAST score 38
 E value 9.0e-12
 Match length 38

09584015-101000

Method BLASTX
 NCBI GI g1346875
 BLAST score 251
 E value 2.0e-21
 Match length 79
 % identity 57
 NCBI Description PHOTOSYSTEM II REACTION CENTER W PROTEIN
 >gi_1185169_emb_CAA91652_ (Z67753) PSII, protein W, 13 kDa
 [Odontella sinensis]

Seq. No. 398976
 Seq. ID LIB3431-020-P1-N1-C2
 Method BLASTN
 NCBI GI g20181
 BLAST score 63
 E value 6.0e-27
 Match length 91
 % identity 92
 NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 398977
 Seq. ID LIB3431-020-P1-N1-C4
 Method BLASTN
 NCBI GI g3789951
 BLAST score 223
 E value 1.0e-122
 Match length 358
 % identity 90
 NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
 (Cab27) mRNA, nuclear gene encoding chloroplast protein,
 complete cds

Seq. No. 398978
 Seq. ID LIB3431-020-P1-N1-C8
 Method BLASTN
 NCBI GI g2072554
 BLAST score 269
 E value 1.0e-149
 Match length 357
 % identity 94
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 398979
 Seq. ID LIB3431-020-P1-N1-C9
 Method BLASTN
 NCBI GI g1519250
 BLAST score 212
 E value 1.0e-115
 Match length 323
 % identity 91
 NCBI Description Oryza sativa GF14-c protein mRNA, complete cds

Seq. No. 398980
 Seq. ID LIB3431-020-P1-N1-D11
 Method BLASTX

09060100 111000

```
Seq. No.          399022
Seq. ID          LIB3431-021-P1-K1-B1
Method           BLASTX
NCBI GI          g4689380
BLAST score      424
E value          8.0e-42
Match length     121
% identity       70
NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein
                  [Vigna radiata]
```

```
Seq. No.      399024
Seq. ID      LIB3431-021-P1-K1-B11
Method       BLASTX
NCBI GI      g132105
BLAST score   657
E value      5.0e-69
Match length  140
% identity    89
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
```


Method BLASTX
 NCBI GI g482311
 BLAST score 571
 E value 4.0e-59
 Match length 115
 % identity 97
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
 (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
 complex protein 1 [Oryza sativa]

Seq. No. 399050
 Seq. ID LIB3431-021-P1-K1-D7
 Method BLASTX
 NCBI GI g1346109
 BLAST score 318
 E value 3.0e-29
 Match length 59
 % identity 100
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
 PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231)
 RWD [Oryza sativa]

Seq. No. 399051
 Seq. ID LIB3431-021-P1-K1-D8
 Method BLASTX
 NCBI GI g131225
 BLAST score 578
 E value 1.0e-59
 Match length 124
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 399052
 Seq. ID LIB3431-021-P1-K1-D9
 Method BLASTX
 NCBI GI g4467099
 BLAST score 482
 E value 2.0e-48
 Match length 119
 % identity 85
 NCBI Description (AL035538) glycine hydroxymethyltransferase like protein
 [Arabidopsis thaliana]

Seq. No. 399053
 Seq. ID LIB3431-021-P1-K1-E1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

09584015.101000

% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 399070
Seq. ID LIB3431-021-P1-K1-G1
Method BLASTN
NCBI GI g304219
BLAST score 53
E value 6.0e-21
Match length 129
% identity 85
NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 399071
Seq. ID LIB3431-021-P1-K1-G10
Method BLASTN
NCBI GI g20262
BLAST score 95
E value 9.0e-46
Match length 190
% identity 88
NCBI Description O.sativa light-induced mRNA

Seq. No. 399072
Seq. ID LIB3431-021-P1-K1-G12
Method BLASTX
NCBI GI g548605
BLAST score 489
E value 2.0e-54
Match length 131
% identity 81
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[Hordeum vulgare]

Seq. No. 399073
Seq. ID LIB3431-021-P1-K1-G2
Method BLASTN
NCBI GI g6015437
BLAST score 35
E value 6.0e-10
Match length 35
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 399074
Seq. ID LIB3431-021-P1-K1-G3
Method BLASTX
NCBI GI g3800878
BLAST score 543
E value 1.0e-55
Match length 150
% identity 71
NCBI Description (AF096281) threonine dehydratase/deaminase [Arabidopsis

% identity 82
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 399113
 Seq. ID LIB3431-021-P1-N1-D9
 Method BLASTN
 NCBI GI g438246
 BLAST score 56
 E value 1.0e-22
 Match length 92
 % identity 90
 NCBI Description S.tuberosum mRNA for glycine hydroxymethyltransferase

Seq. No. 399114
 Seq. ID LIB3431-021-P1-N1-E10
 Method BLASTN
 NCBI GI g1835730
 BLAST score 144
 E value 2.0e-75
 Match length 156
 % identity 98
 NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 399115
 Seq. ID LIB3431-021-P1-N1-E11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 233
 E value 3.0e-19
 Match length 44
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399116
 Seq. ID LIB3431-021-P1-N1-E12
 Method BLASTX
 NCBI GI g3738261
 BLAST score 368
 E value 4.0e-35
 Match length 83
 % identity 92
 NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No. 399117
 Seq. ID LIB3431-021-P1-N1-E4
 Method BLASTX
 NCBI GI g1835731
 BLAST score 252
 E value 1.0e-21
 Match length 65

000101016-97048960

% identity 77
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399118
Seq. ID LIB3431-021-P1-N1-E8
Method BLASTX
NCBI GI g132166
BLAST score 159
E value 8.0e-11
Match length 31
% identity 87
NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
>gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
activase precursor - Arabidopsis thaliana
>gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -
473) [Arabidopsis thaliana]

Seq. No. 399119
Seq. ID LIB3431-021-P1-N1-F1
Method BLASTN
NCBI GI g3789951
BLAST score 77
E value 4.0e-35
Match length 161
% identity 87
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor
(Cab27) mRNA, nuclear gene encoding chloroplast protein,
complete cds

Seq. No. 399120
Seq. ID LIB3431-021-P1-N1-F11
Method BLASTX
NCBI GI g551047
BLAST score 222
E value 4.0e-18
Match length 43
% identity 95
NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 399121
Seq. ID LIB3431-021-P1-N1-F3
Method BLASTX
NCBI GI g2130069
BLAST score 200
E value 2.0e-15
Match length 39
% identity 97
NCBI Description catalase (EC 1.11.1.6) catA - rice
>gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 399122
Seq. ID LIB3431-021-P1-N1-F4
Method BLASTX
NCBI GI g2688822
BLAST score 284
E value 3.0e-25

Match length 98
 % identity 63
 NCBI Description (U93272) pyrophosphate-dependent phosphofructo-1-kinase
 [Prunus armeniaca]

Seq. No. 399123
 Seq. ID LIB3431-021-P1-N1-F6
 Method BLASTX
 NCBI GI g2570515
 BLAST score 196
 E value 6.0e-15
 Match length 41
 % identity 93
 NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 399124
 Seq. ID LIB3431-021-P1-N1-F7
 Method BLASTX
 NCBI GI g3789954
 BLAST score 390
 E value 1.0e-37
 Match length 72
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399125
 Seq. ID LIB3431-021-P1-N1-F8
 Method BLASTX
 NCBI GI g1835731
 BLAST score 173
 E value 2.0e-12
 Match length 49
 % identity 71
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399126
 Seq. ID LIB3431-021-P1-N1-G10
 Method BLASTN
 NCBI GI g20262
 BLAST score 105
 E value 3.0e-52
 Match length 169
 % identity 91
 NCBI Description O.sativa light-induced mRNA

Seq. No. 399127
 Seq. ID LIB3431-021-P1-N1-G3
 Method BLASTX
 NCBI GI g3800878
 BLAST score 206
 E value 4.0e-16
 Match length 58
 % identity 62
 NCBI Description (AF096281) threonine dehydratase/deaminase [Arabidopsis thaliana]


```
Method                BLASTX
NCBI GI                g2501190
BLAST score            240
E value                4.0e-20
Match length           68
% identity              75
NCBI Description        THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                        >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
                        - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                        [Zea mays]
```

```

Seq. No.      399134
Seq. ID       LIB3431-021-P1-N1-H6
Method        BLASTX
NCBI GI       g131176
BLAST score    161
E value       4.0e-11
Match length   32
% identity     97
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
                  (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                  >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
                  barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
                  -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A
                  10.8kD photosystem I protein [Hordeum vulgare var.
                  distichum]

```

```
Seq. No.      399135
Seq. ID      LIB3431-021-P1-N1-H7
Method       BLASTX
NCBI GI      g131225
BLAST score   304
E value      1.0e-27
Match length  75
% identity    77
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]
```

```
Seq. No.      399136
Seq. ID      LIB3431-021-P1-N1-H8
Method       BLASTX
NCBI GI      g5738542
BLAST score   234
E value      1.0e-19
Match length  56
% identity    77
NCBI Description (AJ245867) photosystem I subunit XI precursor [Arabidopsis thaliana]
```

Seq. No.	399137
Seq. ID	LIB3431-021-P1-N1-H9
Method	BLASTX
NCBI GI	g115813
BLAST score	200
E value	2.0e-15

096401F III 0000

```
Seq. No.      399144
Seq. ID      HIB3431-022-P1-K1-A7
Method       BLASTX
NCBI GI      g3345477
BLAST score   544
E value      9.0e-56
Match length  142
% identity    75
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

Seq. No.	399145
Seq. ID	LIB3431-022-P1-K1-A9
Method	BLASTX
NCBI GI	g2245086
BLAST score	373
E value	1.0e-35
Match length	104
% identity	68
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

51017

09684016 "1010000

Match length	84
% identity	67
NCBI Description	(AC004557) F17L21.18 [Arabidopsis thaliana]
Seq. No.	399163
Seq. ID	LIB3431-022-P1-K1-D12
Method	BLASTX
NCBI GI	g3789954
BLAST score	661
E value	2.0e-69
Match length	125
% identity	98
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
Seq. No.	399164
Seq. ID	LIB3431-022-P1-K1-D4
Method	BLASTX
NCBI GI	g320618
BLAST score	593
E value	2.0e-61
Match length	130
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	399165
Seq. ID	LIB3431-022-P1-K1-D5
Method	BLASTX
NCBI GI	g4099148
BLAST score	582
E value	3.0e-60
Match length	147
% identity	82
NCBI Description	(U84268) YLP [Hordeum vulgare]
Seq. No.	399166
Seq. ID	LIB3431-022-P1-K1-D6
Method	BLASTX
NCBI GI	g2293288
BLAST score	175
E value	2.0e-12
Match length	152
% identity	33
NCBI Description	(AF008220) YtcB [Bacillus subtilis] >gi_2635571_emb_CAB15065_ (Z99119) similar to NDP-sugar epimerase [Bacillus subtilis]
Seq. No.	399167
Seq. ID	LIB3431-022-P1-K1-D7
Method	BLASTX
NCBI GI	g5106775
BLAST score	488
E value	3.0e-49

Seq. No.	399178
Seq. ID	LIB3431-022-P1-K1-E9
Method	BLASTN
NCBI GI	g3075487
BLAST score	322
E value	0.0e+00
Match length	322
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

```
Seq. No.      399179
Seq. ID      LIB3431-022-P1-K1-F10
Method       BLASTX
NCBI GI      g2493494
BLAST score   547
E value      4.0e-56
Match length  112
% identity    89
NCBI Description  SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)
                >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase
                [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
                aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase
                II-2 [Hordeum vulgare]
```

```
Seq. No.          399180
Seq. ID           LIB3431-022-P1-K1-F11
Method            BLASTX
NCBI GI           g115787
BLAST score       584
E value           2.0e-60
Match length      133
% identity        88
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      399181
Seq. ID      LIB3431-022-P1-K1-F12
Method       BLASTX
NCBI GI      g3618310
BLAST score   473
E value      2.0e-47
Match length  123
% identity    74
NCBI Description (AB001883) zinc finger protein [Oryza sativa]
```

Seq. No.	399182
Seq. ID	LIB3431-022-P1-K1-F2
Method	BLASTX
NCBI GI	g710626
BLAST score	188
E value	5.0e-14
Match length	45
% identity	69

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chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 399188
Seq. ID LIB3431-022-P1-K1-F9
Method BLASTX
NCBI GI g5295954
BLAST score 363
E value 2.0e-34
Match length 72
% identity 97
NCBI Description (AB026295) hypothetical protein [Oryza sativa]

Seq. No. 399189
Seq. ID LIB3431-022-P1-K1-G10
Method BLASTX
NCBI GI g320618
BLAST score 622
E value 7.0e-65
Match length 135
% identity 87
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 399190
Seq. ID LIB3431-022-P1-K1-G12
Method BLASTN
NCBI GI g2062705
BLAST score 35
E value 5.0e-10
Match length 35
% identity 100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 399191
Seq. ID LIB3431-022-P1-K1-G4
Method BLASTX
NCBI GI g120657
BLAST score 528
E value 6.0e-54
Match length 132
% identity 81
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
CHLOROPLAST >gi_66024_pir_DEZMG3
glyceraldehyde-3-phosphate dehydrogenase (NADP+)
(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)
glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 399192
Seq. ID LIB3431-022-P1-K1-G5
Method BLASTX


```
Method          BLASTX
NCBI GI         g1171978
BLAST score     418
E value        4.0e-45
Match length    128
% identity      63
NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
(PABP 2) >gi_304109 (L19418) poly(A)-binding protein
[Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
poly(A)-binding protein [Arabidopsis thaliana]
```

```
Seq. No.      399198
Seq. ID       LIB3431-022-P1-K1-H12
Method        BLASTX
NCBI GI       g3345477
BLAST score   317
E value       3.0e-29
Match length  115
% identity    57
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

[illegible]

```
Seq. No.      399200
Seq. ID      LIB3431-022-P1-K1-H4
Method       BLASTX
NCBI GI      g3184559
BLAST score   289
E value      7.0e-26
Match length  128
% identity    50
NCBI Description (AF052290) putative c-type cytochrome biogenesis protein
               [Synechococcus PCC7002]
```

```
Seq. No.      399201
Seq. ID       LIB3431-022-P1-K1-H6
Method        BLASTX
NCBI GI       g3510256
BLAST score    180
E value       3.0e-13
Match length   41
% identity     78
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
```

Seq. No. 399202
 Seq. ID LIB3431-022-P1-K1-H7
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 8.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399203
 Seq. ID LIB3431-022-P1-K1-H8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 730
 E value 1.0e-77
 Match length 139
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 399204
 Seq. ID LIB3431-022-P1-N1-A1
 Method BLASTX
 NCBI GI g671740
 BLAST score 202
 E value 1.0e-15
 Match length 51
 % identity 80
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 399205
 Seq. ID LIB3431-022-P1-N1-A4
 Method BLASTX
 NCBI GI g3885892
 BLAST score 235
 E value 1.0e-19
 Match length 47
 % identity 98
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 399206
 Seq. ID LIB3431-022-P1-N1-A5
 Method BLASTX
 NCBI GI g671740
 BLAST score 197
 E value 3.0e-15
 Match length 37
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 399207
 Seq. ID LIB3431-022-P1-N1-A6
 Method BLASTN

Method BLASTN
 NCBI GI g3075487
 BLAST score 42
 E value 3.0e-14
 Match length 82
 % identity 88
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No. 399213
 Seq. ID LIB3431-022-P1-N1-B2
 Method BLASTN
 NCBI GI g218209
 BLAST score 159
 E value 5.0e-84
 Match length 304
 % identity 97
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS2106

Seq. No. 399214
 Seq. ID LIB3431-022-P1-N1-B3
 Method BLASTX
 NCBI GI g4982498
 BLAST score 187
 E value 5.0e-14
 Match length 59
 % identity 59
 NCBI Description (AC000107) F17F8.4 [Arabidopsis thaliana]

Seq. No. 399215
 Seq. ID LIB3431-022-P1-N1-B5
 Method BLASTN
 NCBI GI g3789951
 BLAST score 168
 E value 2.0e-89
 Match length 374
 % identity 93
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor
 (Cab27) mRNA, nuclear gene encoding chloroplast protein,
 complete cds

Seq. No. 399216
 Seq. ID LIB3431-022-P1-N1-B7
 Method BLASTX
 NCBI GI g132105
 BLAST score 402
 E value 4.0e-39
 Match length 73
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

09684015-101000

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399217
Seq. ID LIB3431-022-P1-N1-B9
Method BLASTX
NCBI GI g1125691
BLAST score 180
E value 4.0e-13
Match length 62
% identity 65
NCBI Description (X94301) DnaJ protein [Solanum tuberosum]

Seq. No. 399218
Seq. ID LIB3431-022-P1-N1-C1
Method BLASTX
NCBI GI g4929312
BLAST score 328
E value 2.0e-30
Match length 112
% identity 63
NCBI Description (AF145045) TATC [Arabidopsis thaliana]

Seq. No. 399219
Seq. ID LIB3431-022-P1-N1-C10
Method BLASTN
NCBI GI g6006355
BLAST score 384
E value 0.0e+00
Match length 388
% identity 100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 399220
Seq. ID LIB3431-022-P1-N1-C12
Method BLASTX
NCBI GI g3036951
BLAST score 431
E value 1.0e-42
Match length 81
% identity 100
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]

Seq. No. 399221
Seq. ID LIB3431-022-P1-N1-C2
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. ID LIB3431-022-P1-N1-D5
 Method BLASTX
 NCBI GI g3334409
 BLAST score 204
 E value 5.0e-16
 Match length 52
 % identity 79
 NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
 >gi_2129765_pir_S71261 V-type proton-ATPase - Arabidopsis
 thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type
 proton-ATPase [Arabidopsis thaliana]

Seq. No. 399228
 Seq. ID LIB3431-022-P1-N1-D7
 Method BLASTX
 NCBI GI g5106775
 BLAST score 342
 E value 4.0e-32
 Match length 71
 % identity 92
 NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No. 399229
 Seq. ID LIB3431-022-P1-N1-D8
 Method BLASTX
 NCBI GI g2072555
 BLAST score 226
 E value 2.0e-18
 Match length 46
 % identity 91
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399230
 Seq. ID LIB3431-022-P1-N1-E11
 Method BLASTX
 NCBI GI g4469021
 BLAST score 310
 E value 2.0e-28
 Match length 72
 % identity 81
 NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399231
 Seq. ID LIB3431-022-P1-N1-E12
 Method BLASTX
 NCBI GI g3036946
 BLAST score 277
 E value 2.0e-24
 Match length 52
 % identity 100
 NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein
 [Nicotiana glauca]

Seq. No. 399232
 Seq. ID LIB3431-022-P1-N1-E2

E value 2.0e-24
 Match length 54
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [Nicotiana sylvestris]

Seq. No. 399243
 Seq. ID LIB3431-022-P1-N1-F9
 Method BLASTN
 NCBI GI g5295936
 BLAST score 310
 E value 1.0e-174
 Match length 411
 % identity 94
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
 complete sequence

Seq. No. 399244
 Seq. ID LIB3431-022-P1-N1-G10
 Method BLASTX
 NCBI GI g3928150
 BLAST score 412
 E value 3.0e-40
 Match length 110
 % identity 72
 NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 399245
 Seq. ID LIB3431-022-P1-N1-G4
 Method BLASTX
 NCBI GI g120661
 BLAST score 178
 E value 6.0e-13
 Match length 32
 % identity 100
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
 PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
 dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 399246
 Seq. ID LIB3431-022-P1-N1-G6
 Method BLASTX
 NCBI GI g347451
 BLAST score 263
 E value 7.0e-23
 Match length 51
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
 sativa]

Seq. No. 399247
 Seq. ID LIB3431-022-P1-N1-H11
 Method BLASTX
 NCBI GI g2213871
 BLAST score 195
 E value 7.0e-15
 Match length 53

% identity 83
NCBI Description (AF003126) poly(A)-binding protein [Mesembryanthemum crystallinum]

Seq. No. 399248
Seq. ID LIB3431-022-P1-N1-H12
Method BLASTX
NCBI GI g3345477
BLAST score 156
E value 2.0e-10
Match length 30
% identity 97
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 399249
Seq. ID LIB3431-022-P1-N1-H2
Method BLASTX
NCBI GI g1707998
BLAST score 153
E value 5.0e-10
Match length 29
% identity 100
NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir_S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_(Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 399250
Seq. ID LIB3431-022-P1-N1-H6
Method BLASTX
NCBI GI g3510256
BLAST score 167
E value 1.0e-11
Match length 41
% identity 73
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 399251
Seq. ID LIB3431-022-P1-N1-H7
Method BLASTN
NCBI GI g2072554
BLAST score 310
E value 1.0e-174
Match length 322
% identity 99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 399252
Seq. ID LIB3431-022-P1-N1-H8
Method BLASTX
NCBI GI g115802
BLAST score 190
E value 2.0e-14
Match length 35

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Seq. No.      399254
Seq. ID      LIB3431-023-P1-K1-A11
Method       BLASTX
NCBI GI      g1657621
BLAST score   212
E value      8.0e-17
Match length  109
% identity    54
NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
putative acyl-coA dehydrogenase [Arabidopsis thaliana]
>gi_5478795_dbj_BAA82478.1 (AB017643) Short-chain acyl CoA
oxidase [Arabidopsis thaliana]
```

```
Seq. No.      399256
Seq. ID      LIB3431-023-P1-K1-A4
Method       BLASTX
NCBI GI      g5734618
BLAST score   244
E value      7.0e-27
Match length  154
% identity    44
NCBI Description (AP000391) Similar to Arabidopsis thaliana chromosome II
BAC F5H14 genomic sequence; unknown protein (AC006234)
[Oryza sativa]
```

51039

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NCBI GI      g1173327
BLAST score  227
E value      1.0e-18
Match length 107
% identity   50
NCBI Description
U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')
>gi_322619_pir_S30580 U2 snRNP protein A' - Arabidopsis
thaliana >gi_17669_emb_CAA48890_ (X69137) U2 small nuclear
ribonucleoprotein A' [Arabidopsis thaliana]

```

```
Seq. No.          399258
Seq. ID           LIB3431-023-P1-K1-A6
Method            BLASTX
NCBI GI           g548605
BLAST score       519
E value           1.0e-57
Match length      132
% identity        91
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

Seq. No.	399259
Seq. ID	LIB3431-023-P1-K1-A8
Method	BLASTN
NCBI GI	g2586088
BLAST score	35
E value	5.0e-10
Match length	43
% identity	95
NCBI Description	Oryza longistaminata receptor kinase-like protein, family member A2, pseudogene sequence

```
Seq. No.          399260
Seq. ID           LIB3431-023-P1-K1-A9
Method            BLASTX
NCBI GI           g1052960
BLAST score       400
E value           7.0e-39
Match length      90
% identity        88
NCBI Description   (U37437) PNIL34 [Ipomoea nil]
```

```
Seq. No.      399261
Seq. ID      LIB3431-023-P1-K1-B1
Method       BLASTX
NCBI GI      g6006848
BLAST score   252
E value      2.0e-21
Match length  133
% identity    46
NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis thaliana]
```

Seq. No. 399262

Seq. ID LIB3431-023-P1-K1-B10
 Method BLASTN
 NCBI GI g20153
 BLAST score 157
 E value 8.0e-83
 Match length 157
 % identity 100
 NCBI Description O.sativa random single-copy DNA fragment 12RG143R

Seq. No. 399263
 Seq. ID LIB3431-023-P1-K1-B11
 Method BLASTX
 NCBI GI g3913425
 BLAST score 323
 E value 7.0e-30
 Match length 76
 % identity 79
 NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
 HELICASE >gi_2275203 (AC002337) RNA helicase isolog
 [Arabidopsis thaliana]

Seq. No. 399264
 Seq. ID LIB3431-023-P1-K1-B2
 Method BLASTX
 NCBI GI g2407281
 BLAST score 705
 E value 1.0e-74
 Match length 132
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 399265
 Seq. ID LIB3431-023-P1-K1-B3
 Method BLASTX
 NCBI GI g6016732
 BLAST score 203
 E value 2.0e-18
 Match length 86
 % identity 57
 NCBI Description (AC009325) hypothetical protein [Arabidopsis thaliana]
 >gi_6091719_gb_AAF03431.1_AC010797_7 (AC010797)
 hypothetical protein [Arabidopsis thaliana]

Seq. No. 399266
 Seq. ID LIB3431-023-P1-K1-B5
 Method BLASTN
 NCBI GI g3885887
 BLAST score 419
 E value 0.0e+00
 Match length 442
 % identity 99
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
 complete cds

Seq. No. 399267
 Seq. ID LIB3431-023-P1-K1-B6

Method BLASTX
 NCBI GI g2147484
 BLAST score 592
 E value 2.0e-61
 Match length 137
 % identity 81
 NCBI Description homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
 homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 399268
 Seq. ID LIB3431-023-P1-K1-B9
 Method BLASTX
 NCBI GI g2660676
 BLAST score 614
 E value 5.0e-64
 Match length 134
 % identity 81
 NCBI Description (AC002342) Dreg-2 like protein [Arabidopsis thaliana]

Seq. No. 399269
 Seq. ID LIB3431-023-P1-K1-C1
 Method BLASTX
 NCBI GI g6006848
 BLAST score 405
 E value 2.0e-45
 Match length 141
 % identity 67
 NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No. 399270
 Seq. ID LIB3431-023-P1-K1-C11
 Method BLASTN
 NCBI GI g2306980
 BLAST score 53
 E value 7.0e-21
 Match length 85
 % identity 91
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No. 399271
 Seq. ID LIB3431-023-P1-K1-C12
 Method BLASTX
 NCBI GI g132105
 BLAST score 607
 E value 4.0e-63
 Match length 132
 % identity 87
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate

E value 5.0e-36
 Match length 95
 % identity 75
 NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
 >gi_4874312_gb_AAD31374.1_AC006053_16 (AC006053)
 hypothetical protein [Arabidopsis thaliana]

Seq. No. 399277
 Seq. ID LIB3431-023-P1-K1-C8
 Method BLASTX
 NCBI GI g4803952
 BLAST score 284
 E value 3.0e-25
 Match length 69
 % identity 77
 NCBI Description (AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399278
 Seq. ID LIB3431-023-P1-K1-C9
 Method BLASTX
 NCBI GI g4455350
 BLAST score 322
 E value 1.0e-29
 Match length 79
 % identity 81
 NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 399279
 Seq. ID LIB3431-023-P1-K1-D1
 Method BLASTX
 NCBI GI g2052383
 BLAST score 403
 E value 3.0e-39
 Match length 86
 % identity 80
 NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No. 399280
 Seq. ID LIB3431-023-P1-K1-D10
 Method BLASTX
 NCBI GI g3885892
 BLAST score 440
 E value 1.0e-43
 Match length 83
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 399281
 Seq. ID LIB3431-023-P1-K1-D11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

E value 4.0e-74
Match length 135
% identity 99
NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 399287
Seq. ID LIB3431-023-P1-K1-E11
Method BLASTX
NCBI GI g3789954
BLAST score 778
E value 3.0e-83
Match length 145
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399288
Seq. ID LIB3431-023-P1-K1-E12
Method BLASTX
NCBI GI g517500
BLAST score 270
E value 7.0e-24
Match length 66
% identity 82
NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 399289
Seq. ID LIB3431-023-P1-K1-E3
Method BLASTX
NCBI GI g100849
BLAST score 365
E value 8.0e-49
Match length 128
% identity 75
NCBI Description acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize >gi_22139_emb_CAA45116_ (X63553) acetohydroxyacid synthase [Zea mays]

Seq. No. 399290
Seq. ID LIB3431-023-P1-K1-E5
Method BLASTX
NCBI GI g131225
BLAST score 316
E value 1.0e-56
Match length 122
% identity 91
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 399291
Seq. ID LIB3431-023-P1-K1-E7
Method BLASTN
NCBI GI g6015437

Seq. No. 399306
 Seq. ID LIB3431-023-P1-K1-G8
 Method BLASTX
 NCBI GI g3789954
 BLAST score 639
 E value 6.0e-67
 Match length 119
 % identity 99
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399307
 Seq. ID LIB3431-023-P1-K1-G9
 Method BLASTX
 NCBI GI g132105
 BLAST score 582
 E value 3.0e-60
 Match length 125
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399308
 Seq. ID LIB3431-023-P1-K1-H10
 Method BLASTX
 NCBI GI g120510
 BLAST score 380
 E value 2.0e-36
 Match length 86
 % identity 84
 NCBI Description FERRITIN 2 PRECURSOR >gi_82688_pir_S24057 ferritin precursor (clone FM2) - maize >gi_22278_emb_CAA43664_ (X61392) ferritin [Zea mays]

Seq. No. 399309
 Seq. ID LIB3431-023-P1-K1-H11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 263
 E value 2.0e-28
 Match length 62
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399310
 Seq. ID LIB3431-023-P1-K1-H12
 Method BLASTX

NCBI GI g1835731
 BLAST score 283
 E value 3.0e-25
 Match length 64
 % identity 83
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399311
 Seq. ID LIB3431-023-P1-K1-H3
 Method BLASTX
 NCBI GI g226263
 BLAST score 177
 E value 3.0e-13
 Match length 78
 % identity 53
 NCBI Description chlorophyll a/b binding protein [Glycine max]

Seq. No. 399312
 Seq. ID LIB3431-023-P1-K1-H4
 Method BLASTX
 NCBI GI g871931
 BLAST score 356
 E value 7.0e-34
 Match length 72
 % identity 99
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 399313
 Seq. ID LIB3431-023-P1-K1-H5
 Method BLASTX
 NCBI GI g4850400
 BLAST score 145
 E value 2.0e-19
 Match length 93
 % identity 68
 NCBI Description (AC007357) Similar to gb_M86917 oxysterol-binding protein from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 399314
 Seq. ID LIB3431-023-P1-K1-H6
 Method BLASTX
 NCBI GI g5123939
 BLAST score 242
 E value 5.0e-33
 Match length 102
 % identity 73
 NCBI Description (AL079349) putative protein [Arabidopsis thaliana]

Seq. No. 399315
 Seq. ID LIB3431-023-P1-K1-H8
 Method BLASTX
 NCBI GI g82080
 BLAST score 494
 E value 7.0e-50
 Match length 136
 % identity 69
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 399316
Seq. ID LIB3431-023-P1-K1-H9
Method BLASTX
NCBI GI g3914425
BLAST score 600
E value 2.0e-62
Match length 143
% identity 77
NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
>gi_2511596_emb_CAA74029.1 (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]
>gi_4850389_gb_AAD31059.1_AC007357_8 (AC007357) Identical to gb_Y13695 multicatalytic endopeptidase complex, proteasome precursor, beta subunit (prce) from Arabidopsis thaliana. ESTs gb_Y09360, gb_F13852, gb_T20555, gb_T44620, gb_AI099779 and gb_AA5861

Seq. No. 399317
Seq. ID LIB3431-023-P1-N1-A11
Method BLASTX
NCBI GI g1657621
BLAST score 146
E value 4.0e-09
Match length 36
% identity 81
NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]
>gi_5478795_dbj_BAA82478.1 (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]

Seq. No. 399318
Seq. ID LIB3431-023-P1-N1-A3
Method BLASTN
NCBI GI g5803242
BLAST score 228
E value 1.0e-125
Match length 365
% identity 99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No. 399319
Seq. ID LIB3431-023-P1-N1-A4
Method BLASTX
NCBI GI g5734618
BLAST score 154
E value 4.0e-10
Match length 93
% identity 38
NCBI Description (AP000391) Similar to Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence; unknown protein (AC006234) [Oryza sativa]

Seq. No. 399325
 Seq. ID LIB3431-023-P1-N1-C2
 Method BLASTX
 NCBI GI g231610
 BLAST score 215
 E value 3.0e-17
 Match length 65
 % identity 74
 NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
 >gi_67880_pir_PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No. 399326
 Seq. ID LIB3431-023-P1-N1-C3
 Method BLASTN
 NCBI GI g606816
 BLAST score 301
 E value 1.0e-169
 Match length 321
 % identity 98
 NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No. 399327
 Seq. ID LIB3431-023-P1-N1-C4
 Method BLASTN
 NCBI GI g2072554
 BLAST score 403
 E value 0.0e+00
 Match length 403
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 399328
 Seq. ID LIB3431-023-P1-N1-C5
 Method BLASTX
 NCBI GI g3183079
 BLAST score 629
 E value 1.0e-65
 Match length 147
 % identity 82
 NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
 >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No. 399329
 Seq. ID LIB3431-023-P1-N1-C9
 Method BLASTX
 NCBI GI g731707
 BLAST score 204
 E value 2.0e-22
 Match length 116
 % identity 47
 NCBI Description SET1 PROTEIN >gi_626647_pir_S48961 hypothetical protein

Seq. No. 399344
 Seq. ID LIB3431-023-P1-N1-F5
 Method BLASTX
 NCBI GI g115794
 BLAST score 467
 E value 9.0e-47
 Match length 94
 % identity 91
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No. 399345
 Seq. ID LIB3431-023-P1-N1-F6
 Method BLASTX
 NCBI GI g547712
 BLAST score 219
 E value 1.0e-17
 Match length 43
 % identity 100
 NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir_S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No. 399346
 Seq. ID LIB3431-023-P1-N1-F7
 Method BLASTX
 NCBI GI g347451
 BLAST score 169
 E value 8.0e-12
 Match length 32
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 399347
 Seq. ID LIB3431-023-P1-N1-F9
 Method BLASTX
 NCBI GI g134034
 BLAST score 238
 E value 6.0e-20
 Match length 66
 % identity 68
 NCBI Description 30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5) (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1) >gi_279640_pir_R3SPS5 ribosomal protein CS-S22 precursor, chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270) chloroplast ribosomal protein S22 [Spinacia oleracea] >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein [Spinacia oleracea]

Seq. No. 399348
 Seq. ID LIB3431-023-P1-N1-G10
 Method BLASTX

NCBI GI g421916
 BLAST score 199
 E value 2.0e-15
 Match length 37
 % identity 100
 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
 >gi_12582_emb_CAA48410_ (X68333) light harvesting
 chlorophyll a /b binding protein [Hedera helix]

Seq. No. 399349
 Seq. ID LIB3431-023-P1-N1-G2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399350
 Seq. ID LIB3431-023-P1-N1-G5
 Method BLASTX
 NCBI GI g2130069
 BLAST score 192
 E value 2.0e-14
 Match length 39
 % identity 95
 NCBI Description catalase (EC 1.11.1.6) catA - rice
 >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 399351
 Seq. ID LIB3431-023-P1-N1-G7
 Method BLASTX
 NCBI GI g4972093
 BLAST score 236
 E value 1.0e-19
 Match length 59
 % identity 76
 NCBI Description (AL078468) putative protein [Arabidopsis thaliana]

Seq. No. 399352
 Seq. ID LIB3431-023-P1-N1-G8
 Method BLASTX
 NCBI GI g3789954
 BLAST score 329
 E value 1.0e-30
 Match length 62
 % identity 98
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399353
 Seq. ID LIB3431-023-P1-N1-G9
 Method BLASTX
 NCBI GI g132105

Seq. No. 399363
 Seq. ID LIB3431-024-P1-K1-A4
 Method BLASTN
 NCBI GI g487319
 BLAST score 47
 E value 3.0e-17
 Match length 47
 % identity 100
 NCBI Description Rice mRNA EN66, partial sequence

Seq. No. 399364
 Seq. ID LIB3431-024-P1-K1-A7
 Method BLASTX
 NCBI GI g5902390
 BLAST score 174
 E value 2.0e-12
 Match length 119
 % identity 40
 NCBI Description (AC008148) Unknown protein [Arabidopsis thaliana]

Seq. No. 399365
 Seq. ID LIB3431-024-P1-K1-A9
 Method BLASTX
 NCBI GI g2407281
 BLAST score 673
 E value 6.0e-71
 Match length 125
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 399366
 Seq. ID LIB3431-024-P1-K1-B1
 Method BLASTX
 NCBI GI g132105
 BLAST score 530
 E value 4.0e-54
 Match length 96
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399367
 Seq. ID LIB3431-024-P1-K1-B10
 Method BLASTX
 NCBI GI g729478
 BLAST score 343
 E value 3.0e-32
 Match length 119

Method BLASTX
 NCBI GI g4884866
 BLAST score 275
 E value 2.0e-24
 Match length 96
 % identity 57
 NCBI Description (AF133531) water channel protein MipI [Mesembryanthemum crystallinum]

Seq. No. 399383
 Seq. ID LIB3431-024-P1-K1-C7
 Method BLASTX
 NCBI GI g3402713
 BLAST score 248
 E value 5.0e-21
 Match length 64
 % identity 72
 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399384
 Seq. ID LIB3431-024-P1-K1-C8
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399385
 Seq. ID LIB3431-024-P1-K1-C9
 Method BLASTN
 NCBI GI g20181
 BLAST score 58
 E value 5.0e-24
 Match length 62
 % identity 98
 NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No. 399386
 Seq. ID LIB3431-024-P1-K1-D1
 Method BLASTX
 NCBI GI g3913641
 BLAST score 483
 E value 6.0e-49
 Match length 95
 % identity 98
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_3041777_dbj_BAA25423_ (AB007194)
 fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 399387
 Seq. ID LIB3431-024-P1-K1-D10

Method	BLASTX
NCBI GI	g4689380
BLAST score	620
E value	9.0e-65
Match length	125
% identity	88
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]
Seq. No.	399388
Seq. ID	LIB3431-024-P1-K1-D12
Method	BLASTX
NCBI GI	g320618
BLAST score	463
E value	2.0e-46
Match length	106
% identity	83
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	399389
Seq. ID	LIB3431-024-P1-K1-D2
Method	BLASTN
NCBI GI	g2306980
BLAST score	150
E value	7.0e-79
Match length	174
% identity	97
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds
Seq. No.	399390
Seq. ID	LIB3431-024-P1-K1-D3
Method	BLASTX
NCBI GI	g871931
BLAST score	361
E value	1.0e-36
Match length	85
% identity	100
NCBI Description	(D30763) ferredoxin [Oryza sativa]
Seq. No.	399391
Seq. ID	LIB3431-024-P1-K1-D4
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	399392
Seq. ID	LIB3431-024-P1-K1-D6
Method	BLASTX

NCBI GI	g2342719
BLAST score	324
E value	6.0e-30
Match length	139
% identity	50
NCBI Description	(AC002341) SF16 protein isolog [Arabidopsis thaliana]
Seq. No.	399393
Seq. ID	LIB3431-024-P1-K1-D9
Method	BLASTX
NCBI GI	g4585882
BLAST score	399
E value	7.0e-39
Match length	127
% identity	62
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	399394
Seq. ID	LIB3431-024-P1-K1-E1
Method	BLASTX
NCBI GI	g2407281
BLAST score	547
E value	3.0e-56
Match length	108
% identity	96
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]
Seq. No.	399395
Seq. ID	LIB3431-024-P1-K1-E10
Method	BLASTX
NCBI GI	g133936
BLAST score	685
E value	3.0e-72
Match length	132
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3 ribosomal protein S3 - rice chloroplast >gi_12025_emb_CAA33934_(X15901) ribosomal protein S3 [Oryza sativa] >gi_226646_prf__1603356BW ribosomal protein S3 [Oryza sativa]
Seq. No.	399396
Seq. ID	LIB3431-024-P1-K1-E12
Method	BLASTX
NCBI GI	g2130069
BLAST score	749
E value	8.0e-80
Match length	135
% identity	99
NCBI Description	catalase (EC 1.11.1.6) cataA - rice >gi_1261858_dbj_BAA06232_(D29966) catalase [Oryza sativa]
Seq. No.	399397
Seq. ID	LIB3431-024-P1-K1-E2
Method	BLASTX


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Method          BLASTX
NCBI GI         g5902158
BLAST score     246
E value         6.0e-21
Match length    75
% identity      56
NCBI Description zinc finger protein 183 (RING finger, C3HC4 type)
                >gi_3123165_sp_015541_z183_HUMAN_ZINC_FINGER_PROTEIN_183
                >gi_2274982_emb_CAA66907_(X98253) ZNF183 [Homo sapiens]
                >gi_2341022_(AC002477) zinc-finger protein [Homo sapiens]
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Seq. No.      399414
Seq. ID      LIB3431-024-P1-K1-G2
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      6.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
                >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                protein [Oryza sativa]
```

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Seq. No.      399415
Seq. ID      LIB3431-024-P1-K1-G4
Method       BLASTX
NCBI GI      g115787
BLAST score   380
E value      1.0e-36
Match length  92
% identity    85
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

Seq. No.	399416
Seq. ID	LIB3431-024-P1-K1-G6
Method	BLASTX
NCBI GI	g1657859
BLAST score	155
E value	2.0e-10
Match length	60
% identity	55
NCBI Description	(U73218) chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]

```
Seq. No.      399417
Seq. ID      LIB3431-024-P1-K1-G7
Method       BLASTX
NCBI GI      g3386621
BLAST score   554
E value      6.0e-57
Match length  147
% identity    71
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
```

Seq. No. 399418
 Seq. ID LIB3431-024-P1-K1-G8
 Method BLASTX
 NCBI GI g4538947
 BLAST score 166
 E value 1.0e-11
 Match length 61
 % identity 54
 NCBI Description (AL049483) putative mitochondrial carrier protein
 [Arabidopsis thaliana]

Seq. No. 399419
 Seq. ID LIB3431-024-P1-K1-G9
 Method BLASTX
 NCBI GI g132105
 BLAST score 289
 E value 4.0e-26
 Match length 76
 % identity 78
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 399420
 Seq. ID LIB3431-024-P1-K1-H1
 Method BLASTX
 NCBI GI g3885886
 BLAST score 327
 E value 8.0e-31
 Match length 65
 % identity 100
 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 399421
 Seq. ID LIB3431-024-P1-K1-H11
 Method BLASTX
 NCBI GI g1931644
 BLAST score 250
 E value 3.0e-21
 Match length 105
 % identity 44
 NCBI Description (U95973) membrane protein PTM1 precursor isolog
 [Arabidopsis thaliana]

Seq. No. 399422
 Seq. ID LIB3431-024-P1-K1-H12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 8.0e-20

Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399423
 Seq. ID LIB3431-024-P1-K1-H2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 6.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399424
 Seq. ID LIB3431-024-P1-K1-H3
 Method BLASTX
 NCBI GI g1835731
 BLAST score 189
 E value 3.0e-14
 Match length 49
 % identity 76
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399425
 Seq. ID LIB3431-024-P1-K1-H4
 Method BLASTX
 NCBI GI g1498315
 BLAST score 250
 E value 7.0e-25
 Match length 121
 % identity 50
 NCBI Description (U56419) IAP100 [Pisum sativum]

Seq. No. 399426
 Seq. ID LIB3431-024-P1-K1-H5
 Method BLASTX
 NCBI GI g1617197
 BLAST score 290
 E value 6.0e-26
 Match length 76
 % identity 74
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399427
 Seq. ID LIB3431-024-P1-K1-H6
 Method BLASTN
 NCBI GI g3821780
 BLAST score 34
 E value 9.0e-10
 Match length 34
 % identity 100
 NCBI Description Xenopus laevis cDNA clone 27A6-1

BLAST score 370
 E value 2.0e-35
 Match length 73
 % identity 92
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
 reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
 (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
 a region of the predicted gene.; similar to
 ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 399433
 Seq. ID LIB3431-024-P1-N1-B12
 Method BLASTX
 NCBI GI g132166
 BLAST score 156
 E value 2.0e-10
 Match length 31
 % identity 84
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
 activase precursor - Arabidopsis thaliana
 >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -
 473) [Arabidopsis thaliana]

Seq. No. 399434
 Seq. ID LIB3431-024-P1-N1-B2
 Method BLASTX
 NCBI GI g417260
 BLAST score 268
 E value 2.0e-23
 Match length 69
 % identity 72
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 399435
 Seq. ID LIB3431-024-P1-N1-B4
 Method BLASTX
 NCBI GI g3789954
 BLAST score 335
 E value 3.0e-31
 Match length 62
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 399436
 Seq. ID LIB3431-024-P1-N1-B5
 Method BLASTX
 NCBI GI g131225
 BLAST score 196
 E value 5.0e-15
 Match length 51
 % identity 73

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 399437
 Seq. ID LIB3431-024-P1-N1-B6
 Method BLASTX
 NCBI GI g2072555
 BLAST score 196
 E value 5.0e-15
 Match length 37
 % identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399438
 Seq. ID LIB3431-024-P1-N1-B8
 Method BLASTX
 NCBI GI g131225
 BLAST score 216
 E value 2.0e-17
 Match length 56
 % identity 73

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 399439
 Seq. ID LIB3431-024-P1-N1-B9
 Method BLASTX
 NCBI GI g1835731
 BLAST score 590
 E value 4.0e-61
 Match length 126
 % identity 91

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399440
 Seq. ID LIB3431-024-P1-N1-C1
 Method BLASTX
 NCBI GI g4512616
 BLAST score 334
 E value 3.0e-31
 Match length 80
 % identity 81

NCBI Description (AC004793) Contains similarity to gi_1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb_D90912 and is a member of the Inositol monophosphatase family PF_00459. EST gb_AA597395 comes from this gene. [Arabidopsis tha

Seq. No. 399441
 Seq. ID LIB3431-024-P1-N1-C10
 Method BLASTX
 NCBI GI g2407279

0001016-101000

BLAST score 216
E value 2.0e-17
Match length 44
% identity 100
NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 399442
Seq. ID LIB3431-024-P1-N1-C11
Method BLASTX
NCBI GI g3036946
BLAST score 319
E value 2.0e-29
Match length 61
% identity 100
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 399443
Seq. ID LIB3431-024-P1-N1-C12
Method BLASTX
NCBI GI g1835731
BLAST score 188
E value 3.0e-14
Match length 48
% identity 77
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399444
Seq. ID LIB3431-024-P1-N1-C3
Method BLASTX
NCBI GI g3036942
BLAST score 243
E value 1.0e-20
Match length 45
% identity 100
NCBI Description (AB012636) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 399445
Seq. ID LIB3431-024-P1-N1-C8
Method BLASTN
NCBI GI g2072554
BLAST score 246
E value 1.0e-136
Match length 282
% identity 97
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 399446
Seq. ID LIB3431-024-P1-N1-D1
Method BLASTX
NCBI GI g3913641
BLAST score 211
E value 4.0e-17
Match length 41
% identity 100

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
>gi_3041777_dbj_BAA25423_ (AB007194)
fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 399447
Seq. ID LIB3431-024-P1-N1-D10
Method BLASTX
NCBI GI g479406
BLAST score 396
E value 2.0e-38
Match length 78
% identity 95

NCBI Description chlorophyll a/b-binding protein - garden pea
>gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
protein [Pisum sativum]

Seq. No. 399448
Seq. ID LIB3431-024-P1-N1-D11
Method BLASTX
NCBI GI g3510256
BLAST score 194
E value 7.0e-15
Match length 48
% identity 67
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 399449
Seq. ID LIB3431-024-P1-N1-D12
Method BLASTX
NCBI GI g115787
BLAST score 432
E value 1.0e-42
Match length 82
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109_
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 399450
Seq. ID LIB3431-024-P1-N1-D2
Method BLASTX
NCBI GI g551047
BLAST score 268
E value 2.0e-23
Match length 52
% identity 96
NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 399451
Seq. ID LIB3431-024-P1-N1-D3
Method BLASTN
NCBI GI g2305114
BLAST score 291
E value 1.0e-163

0968401E-701000

```
Seq. No.      399458
Seq. ID      LIB3431-024-P1-N1-E8
Method       BLASTX
NCBI GI      g3126854
BLAST score   240
E value      3.0e-20
Match length  65
% identity    74
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

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Seq. No.      399460
Seq. ID      LIB3431-024-P1-N1-F10
Method       BLASTX
NCBI GI      g3126854
BLAST score   261
E value      1.0e-22
Match length  52
% identity    94
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
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Seq. No.      399462
Seq. ID      LIB3431-024-P1-N1-F2
Method       BLASTN
NCBI GI      q5360229
```

BLAST score 394
E value 0.0e+00
Match length 419
% identity 98
NCBI Description Oryza sativa mRNA for Ran, complete cds

Seq. No. 399463
Seq. ID LIB3431-024-P1-N1-F3
Method BLASTN
NCBI GI g3789949
BLAST score 83
E value 1.0e-38
Match length 95
% identity 97
NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No. 399464
Seq. ID LIB3431-024-P1-N1-F4
Method BLASTX
NCBI GI g4582436
BLAST score 162
E value 7.0e-11
Match length 77
% identity 47
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]

Seq. No. 399465
Seq. ID LIB3431-024-P1-N1-F7
Method BLASTX
NCBI GI g4929312
BLAST score 203
E value 7.0e-16
Match length 70
% identity 63
NCBI Description (AF145045) TATC [Arabidopsis thaliana]

Seq. No. 399466
Seq. ID LIB3431-024-P1-N1-G10
Method BLASTX
NCBI GI g4731573
BLAST score 201
E value 1.0e-15
Match length 48
% identity 77
NCBI Description (AF123265) remorin 1 [Lycopersicon esculentum]

Seq. No. 399467
Seq. ID LIB3431-024-P1-N1-G12
Method BLASTX
NCBI GI g5262156
BLAST score 226
E value 2.0e-18
Match length 65
% identity 52
NCBI Description (AL080237) putative protein [Arabidopsis thaliana]

000101-91018360

05634010 101000

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Seq. No.      399474
Seq. ID      LIB3431-024-P1-N1-H12
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      9.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

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Seq. No.      399476
Seq. ID      LIB3431-024-P1-N1-H3
Method       BLASTX
NCBI GI      g1835731
BLAST score   189
E value      3.0e-14
Match length  49
% identity    78
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```


Seq. No. 399483
 Seq. ID LIB3431-025-P1-K1-A8
 Method BLASTX
 NCBI GI g2501491
 BLAST score 182
 E value 1.0e-13
 Match length 90
 % identity 42
 NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 1) >gi_542014_pir__S41950
 UTP-glucose glucosyltransferase - cassava
 >gi_453246_emb_CAA54609_(X77459) UTP-glucose
 glucosyltransferase [Manihot esculenta]

Seq. No. 399484
 Seq. ID LIB3431-025-P1-K1-B11
 Method BLASTX
 NCBI GI g671740
 BLAST score 433
 E value 1.0e-42
 Match length 79
 % identity 99
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 399485
 Seq. ID LIB3431-025-P1-K1-B2
 Method BLASTX
 NCBI GI g1362184
 BLAST score 447
 E value 4.0e-44
 Match length 91
 % identity 100
 NCBI Description histone H2B-8 - wheat >gi_531058_dbj_BAA07157_(D37943)
 protein H2B-8 [Triticum aestivum]

Seq. No. 399486
 Seq. ID LIB3431-025-P1-K1-B3
 Method BLASTX
 NCBI GI g1076800
 BLAST score 681
 E value 1.0e-71
 Match length 148
 % identity 86
 NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
 maize >gi_600116_emb_CAA84406_(Z34934) cytosolic ascorbate
 peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
 peroxidase [Zea mays]

Seq. No. 399487
 Seq. ID LIB3431-025-P1-K1-B5
 Method BLASTX
 NCBI GI g3868756
 BLAST score 842
 E value 2.0e-90
 Match length 154
 % identity 100

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Seq. No. 399498
Seq. ID LIB3431-025-P1-K1-D8
Method BLASTX
NCBI GI g2055273
BLAST score 1024
E value 1.0e-112
Match length 236
% identity 83
NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No. 399499
Seq. ID LIB3431-025-P1-K1-D9
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399500
Seq. ID LIB3431-025-P1-K1-E11
Method BLASTX
NCBI GI g347451
BLAST score 459
E value 1.0e-57
Match length 165
% identity 74
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 399501
Seq. ID LIB3431-025-P1-K1-E12
Method BLASTX
NCBI GI g2582822
BLAST score 606
E value 7.0e-63
Match length 168
% identity 71
NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No. 399502
Seq. ID LIB3431-025-P1-K1-E5
Method BLASTX
NCBI GI g462195
BLAST score 524
E value 4.0e-53
Match length 115
% identity 89
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
>gi_100682_pir_S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza

sativa]

Seq. No. 399503
 Seq. ID LIB3431-025-P1-K1-E6
 Method BLASTX
 NCBI GI g2425101
 BLAST score 798
 E value 3.0e-85
 Match length 215
 % identity 64
 NCBI Description (AF019743) cationic peroxidase [Oryza sativa]

Seq. No. 399504
 Seq. ID LIB3431-025-P1-K1-E7
 Method BLASTN
 NCBI GI g1841354
 BLAST score 66
 E value 2.0e-29
 Match length 66
 % identity 100
 NCBI Description Oryza sativa mitochondrial DNA for cytochrome c oxidase subunit Vb precursor, complete cds

Seq. No. 399505
 Seq. ID LIB3431-025-P1-K1-E9
 Method BLASTX
 NCBI GI g3913239
 BLAST score 406
 E value 2.0e-39
 Match length 146
 % identity 58
 NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No. 399506
 Seq. ID LIB3431-025-P1-K1-F10
 Method BLASTX
 NCBI GI g1084455
 BLAST score 503
 E value 8.0e-51
 Match length 118
 % identity 81
 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 399507
 Seq. ID LIB3431-025-P1-K1-F11
 Method BLASTX
 NCBI GI g1777961
 BLAST score 958
 E value 1.0e-104
 Match length 233
 % identity 76
 NCBI Description (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No. 399508
 Seq. ID LIB3431-025-P1-K1-F12
 Method BLASTX
 NCBI GI g400803
 BLAST score 509
 E value 3.0e-64
 Match length 154
 % identity 82
 NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_283033_pir_A42807 phosphoglycerate mutase (EC 5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Seq. No. 399509
 Seq. ID LIB3431-025-P1-K1-F2
 Method BLASTX
 NCBI GI g132105
 BLAST score 423
 E value 2.0e-41
 Match length 81
 % identity 96
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399510
 Seq. ID LIB3431-025-P1-K1-F3
 Method BLASTX
 NCBI GI g4467098
 BLAST score 324
 E value 1.0e-29
 Match length 136
 % identity 44
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 399511
 Seq. ID LIB3431-025-P1-K1-F5
 Method BLASTX
 NCBI GI g6093671
 BLAST score 388
 E value 2.0e-37
 Match length 122
 % identity 61
 NCBI Description CATIONIC PEROXIDASE 1 PRECURSOR >gi_1491776 (M37636) cationic peroxidase [Arachis hypogaea]

Seq. No. 399512
 Seq. ID LIB3431-025-P1-K1-F6
 Method BLASTX

NCBI GI g1617197
 BLAST score 304
 E value 2.0e-27
 Match length 76
 % identity 76
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399513
 Seq. ID LIB3431-025-P1-K1-F7
 Method BLASTX
 NCBI GI g4938484
 BLAST score 326
 E value 6.0e-30
 Match length 205
 % identity 45
 NCBI Description (AL078464) transcription factor-like protein [Arabidopsis thaliana]

Seq. No. 399514
 Seq. ID LIB3431-025-P1-K1-F8
 Method BLASTX
 NCBI GI g1706260
 BLAST score 355
 E value 2.0e-33
 Match length 68
 % identity 94
 NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
 cysteine proteinase 1 precursor - maize
 >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No. 399515
 Seq. ID LIB3431-025-P1-K1-F9
 Method BLASTX
 NCBI GI g5815410
 BLAST score 828
 E value 4.0e-94
 Match length 209
 % identity 83
 NCBI Description (AF177392) blast and wounding induced mitogen-activated protein kinase [Oryza sativa]

Seq. No. 399516
 Seq. ID LIB3431-025-P1-K1-G10
 Method BLASTX
 NCBI GI g1653953
 BLAST score 212
 E value 6.0e-17
 Match length 130
 % identity 38
 NCBI Description (D90917) hypothetical protein [Synechocystis sp.]

Seq. No. 399517
 Seq. ID LIB3431-025-P1-K1-G9
 Method BLASTX
 NCBI GI g3789954
 BLAST score 1065

E value 1.0e-116
 Match length 199
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399518
 Seq. ID LIB3431-025-P1-K1-H10
 Method BLASTX
 NCBI GI g1737492
 BLAST score 626
 E value 4.0e-65
 Match length 177
 % identity 71
 NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 399519
 Seq. ID LIB3431-025-P1-K1-H3
 Method BLASTX
 NCBI GI g3913641
 BLAST score 1185
 E value 1.0e-130
 Match length 227
 % identity 100
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_3041777_dbj_BAA25423_ (AB007194)
 fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 399520
 Seq. ID LIB3431-025-P1-K1-H4
 Method BLASTX
 NCBI GI g4678280
 BLAST score 259
 E value 5.0e-22
 Match length 152
 % identity 36
 NCBI Description (AL049660) zinc finger-like protein [Arabidopsis thaliana]

Seq. No. 399521
 Seq. ID LIB3431-025-P1-K1-H7
 Method BLASTX
 NCBI GI g115787
 BLAST score 544
 E value 1.0e-107
 Match length 224
 % identity 91
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 399522
 Seq. ID LIB3431-025-P1-K1-H9
 Method BLASTX
 NCBI GI g3036951

BLAST score 611
 E value 2.0e-63
 Match length 117
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [Nicotiana sylvestris]

Seq. No. 399523
 Seq. ID LIB3431-025-P1-N1-A1
 Method BLASTX
 NCBI GI g3885882
 BLAST score 275
 E value 3.0e-24
 Match length 55
 % identity 98
 NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No. 399524
 Seq. ID LIB3431-025-P1-N1-A11
 Method BLASTX
 NCBI GI g3808101
 BLAST score 303
 E value 1.0e-27
 Match length 73
 % identity 88
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 399525
 Seq. ID LIB3431-025-P1-N1-A12
 Method BLASTN
 NCBI GI g2072554
 BLAST score 330
 E value 0.0e+00
 Match length 330
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 399526
 Seq. ID LIB3431-025-P1-N1-A5
 Method BLASTN
 NCBI GI g395929
 BLAST score 82
 E value 5.0e-38
 Match length 145
 % identity 90
 NCBI Description O.sativa retrotransposon Tos1-1

Seq. No. 399527
 Seq. ID LIB3431-025-P1-N1-A7
 Method BLASTX
 NCBI GI g693920
 BLAST score 340
 E value 6.0e-32
 Match length 68
 % identity 96
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum

09816101000

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Seq. No.      399529
Seq. ID      LIB3431-025-P1-N1-B1
Method       BLASTN
NCBI GI      g5091597
BLAST score   132
E value      6.0e-68
Match length  219
% identity    26
NCBI Description  Oryza sativa chromosome 1 BAC 10A19I, complete sequence
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Seq. No.      399531
Seq. ID       LIB3431-025-P1-N1-B11
Method        BLASTX
NCBI GI       g671740
BLAST score    295
E value       1.0e-26
Match length   57
% identity     98
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

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% identity 99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 399538
Seq. ID LIB3431-025-P1-N1-C6
Method BLASTX
NCBI GI g2072555
BLAST score 228
E value 1.0e-18
Match length 42
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399539
Seq. ID LIB3431-025-P1-N1-C7
Method BLASTX
NCBI GI g3914466
BLAST score 395
E value 2.0e-38
Match length 72
% identity 99
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
(PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays]

Seq. No. 399540
Seq. ID LIB3431-025-P1-N1-C9
Method BLASTX
NCBI GI g517500
BLAST score 374
E value 7.0e-36
Match length 90
% identity 81
NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 399541
Seq. ID LIB3431-025-P1-N1-D1
Method BLASTX
NCBI GI g1353352
BLAST score 227
E value 1.0e-18
Match length 59
% identity 75
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 399542
Seq. ID LIB3431-025-P1-N1-D10
Method BLASTX
NCBI GI g3126854
BLAST score 392
E value 5.0e-38
Match length 74

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% identity      100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.        399543
Seq. ID         LIB3431-025-P1-N1-D11
Method          BLASTX
NCBI GI         g5091556
BLAST score     194
E value         9.0e-15
Match length    55
% identity      58
NCBI Description (AC007067) T10024.25 [Arabidopsis thaliana]

Seq. No.        399544
Seq. ID         LIB3431-025-P1-N1-D12
Method          BLASTX
NCBI GI         g1841466
BLAST score     182
E value         2.0e-13
Match length    32
% identity      94
NCBI Description (Y11003) putative pre-pro-cysteine proteinase [Nicotiana
tabacum]

Seq. No.        399545
Seq. ID         LIB3431-025-P1-N1-D2
Method          BLASTX
NCBI GI         g4587990
BLAST score     250
E value         2.0e-21
Match length    88
% identity      50
NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.        399546
Seq. ID         LIB3431-025-P1-N1-D4
Method          BLASTX
NCBI GI         g2598151
BLAST score     222
E value         5.0e-18
Match length    43
% identity      95
NCBI Description (AF027350) NADPH:protochlorophyllide oxidoreductase porB
[Pinus taeda]

Seq. No.        399547
Seq. ID         LIB3431-025-P1-N1-D7
Method          BLASTX
NCBI GI         g417260
BLAST score     300
E value         3.0e-27
Match length    76
% identity      75
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
light-regulated gene [Oryza sativa]

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sativa]

Seq. No. 399553
 Seq. ID LIB3431-025-P1-N1-E6
 Method BLASTN
 NCBI GI g5777612
 BLAST score 407
 E value 0.0e+00
 Match length 418
 % identity 99
 NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No. 399554
 Seq. ID LIB3431-025-P1-N1-E7
 Method BLASTN
 NCBI GI g1841354
 BLAST score 66
 E value 2.0e-29
 Match length 66
 % identity 100
 NCBI Description Oryza sativa mitochondrial DNA for cytochrome c oxidase subunit Vb precursor, complete cds

Seq. No. 399555
 Seq. ID LIB3431-025-P1-N1-E8
 Method BLASTX
 NCBI GI g3036951
 BLAST score 427
 E value 4.0e-42
 Match length 80
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 399556
 Seq. ID LIB3431-025-P1-N1-E9
 Method BLASTX
 NCBI GI g3913239
 BLAST score 256
 E value 4.0e-40
 Match length 132
 % identity 75
 NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No. 399557
 Seq. ID LIB3431-025-P1-N1-F10
 Method BLASTN
 NCBI GI g600766
 BLAST score 296
 E value 1.0e-166
 Match length 364
 % identity 95
 NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

Seq. No. 399558

Seq. ID LIB3431-025-P1-N1-F11
 Method BLASTX
 NCBI GI g1777961
 BLAST score 342
 E value 4.0e-32
 Match length 114
 % identity 61
 NCBI Description (U56406) methyljasmonate-inducible lipxygenase 2 [Hordeum vulgare]

Seq. No. 399559
 Seq. ID LIB3431-025-P1-N1-F2
 Method BLASTX
 NCBI GI g347451
 BLAST score 236
 E value 1.0e-19
 Match length 47
 % identity 98
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 399560
 Seq. ID LIB3431-025-P1-N1-F5
 Method BLASTX
 NCBI GI g520568
 BLAST score 262
 E value 1.0e-22
 Match length 87
 % identity 63
 NCBI Description (U12314) peroxidase [Cenchrus ciliaris]

Seq. No. 399561
 Seq. ID LIB3431-025-P1-N1-F6
 Method BLASTX
 NCBI GI g1617197
 BLAST score 287
 E value 1.0e-25
 Match length 71
 % identity 73
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399562
 Seq. ID LIB3431-025-P1-N1-F8
 Method BLASTX
 NCBI GI g2118130
 BLAST score 255
 E value 7.0e-22
 Match length 47
 % identity 94
 NCBI Description cysteine proteinase (EC 3.4.22.-), glucose starvation-induced - maize (fragment)
 >gi_559532_emb_CAA57675_ (X82185) cysteine proteinase [Zea mays]

Seq. No. 399563
 Seq. ID LIB3431-025-P1-N1-F9
 Method BLASTN

NCBI GI g5815409
 BLAST score 420
 E value 0.0e+00
 Match length 449
 % identity 98
 NCBI Description Oryza sativa blast and wounding induced mitogen-activated protein kinase (BWMK1) mRNA, complete cds

Seq. No. 399564
 Seq. ID LIB3431-025-P1-N1-G10
 Method BLASTX
 NCBI GI g1653953
 BLAST score 190
 E value 3.0e-14
 Match length 91
 % identity 42
 NCBI Description (D90917) hypothetical protein [Synechocystis sp.]

Seq. No. 399565
 Seq. ID LIB3431-025-P1-N1-G11
 Method BLASTX
 NCBI GI g2130073
 BLAST score 308
 E value 4.0e-28
 Match length 60
 % identity 100
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 399566
 Seq. ID LIB3431-025-P1-N1-G12
 Method BLASTN
 NCBI GI g786177
 BLAST score 55
 E value 4.0e-22
 Match length 130
 % identity 86
 NCBI Description Rice DNA for aldolase C-1, complete cds

Seq. No. 399567
 Seq. ID LIB3431-025-P1-N1-G3
 Method BLASTX
 NCBI GI g2708745
 BLAST score 197
 E value 3.0e-15
 Match length 48
 % identity 81
 NCBI Description (AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No. 399568
 Seq. ID LIB3431-025-P1-N1-G5
 Method BLASTX
 NCBI GI g21839
 BLAST score 229

E value 7.0e-19
 Match length 47
 % identity 96
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 399569
 Seq. ID LIB3431-025-P1-N1-G9
 Method BLASTX
 NCBI GI g3789954
 BLAST score 354
 E value 2.0e-33
 Match length 66
 % identity 98
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399570
 Seq. ID LIB3431-025-P1-N1-H10
 Method BLASTX
 NCBI GI g1737492
 BLAST score 280
 E value 6.0e-25
 Match length 70
 % identity 80
 NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 399571
 Seq. ID LIB3431-025-P1-N1-H12
 Method BLASTX
 NCBI GI g517500
 BLAST score 296
 E value 8.0e-27
 Match length 94
 % identity 67
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 399572
 Seq. ID LIB3431-025-P1-N1-H2
 Method BLASTX
 NCBI GI g1651922
 BLAST score 176
 E value 1.0e-12
 Match length 59
 % identity 56
 NCBI Description (D90901) hypothetical protein [Synechocystis sp.]

Seq. No. 399573
 Seq. ID LIB3431-025-P1-N1-H3
 Method BLASTX
 NCBI GI g3913641
 BLAST score 529
 E value 5.0e-54
 Match length 100
 % identity 100
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
>gi_3041777_dbj_BAA25423_ (AB007194)
fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 399574
Seq. ID LIB3431-025-P1-N1-H5
Method BLASTX
NCBI GI g129707
BLAST score 419
E value 4.0e-41
Match length 95
% identity 86
NCBI Description PROTOCHLOROPHYLLIDE REDUCTASE (PCR)
(NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE)
>gi_100550_pir_S08406 protochlorophyllide reductase (EC
1.3.1.33) - oat (fragment) >gi_829253_emb_CAA34913_
(X17067) protochlorophyllide reductase (314 AA) [Avena
sativa]

Seq. No. 399575
Seq. ID LIB3431-025-P1-N1-H7
Method BLASTX
NCBI GI g4512125
BLAST score 243
E value 1.0e-20
Match length 45
% identity 100
NCBI Description (AF133340) putative chlorophyll a/b-binding protein
[Phalaenopsis sp. 'KCbutterfly']

Seq. No. 399576
Seq. ID LIB3431-025-P1-N1-H8
Method BLASTX
NCBI GI g267120
BLAST score 284
E value 2.0e-25
Match length 71
% identity 77
NCBI Description THIOREDOXIN F-TYPE, CHLOROPLAST PRECURSOR (TRX-F)
>gi_100070_pir_S20929 thioredoxin f precursor - garden pea
>gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum
sativum] >gi_1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No. 399577
Seq. ID LIB3431-025-P1-N1-H9
Method BLASTX
NCBI GI g3036951
BLAST score 450
E value 9.0e-45
Match length 85
% identity 100
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
[Nicotiana glauca]

Seq. No. 399578
Seq. ID LIB3431-026-P1-K1-A1
Method BLASTX

E value 8.0e-39
 Match length 98
 % identity 77
 NCBI Description IN2-2 PROTEIN

Seq. No. 399584
 Seq. ID LIB3431-026-P1-K1-A4
 Method BLASTX
 NCBI GI g132105
 BLAST score 672
 E value 7.0e-71
 Match length 124
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399585
 Seq. ID LIB3431-026-P1-K1-A5
 Method BLASTX
 NCBI GI g3345477
 BLAST score 269
 E value 1.0e-23
 Match length 98
 % identity 58
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 399586
 Seq. ID LIB3431-026-P1-K1-A6
 Method BLASTX
 NCBI GI g4538920
 BLAST score 150
 E value 1.0e-09
 Match length 57
 % identity 60
 NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No. 399587
 Seq. ID LIB3431-026-P1-K1-A7
 Method BLASTN
 NCBI GI g218209
 BLAST score 34
 E value 1.0e-09
 Match length 78
 % identity 87
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 399588

Method BLASTX
 NCBI GI g3868756
 BLAST score 494
 E value 3.0e-50
 Match length 88
 % identity 100
 NCBI Description (D86611) catalase [Oryza sativa]

Seq. No. 399599
 Seq. ID LIB3431-026-P1-K1-C1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399600
 Seq. ID LIB3431-026-P1-K1-C10
 Method BLASTX
 NCBI GI g5668640
 BLAST score 515
 E value 2.0e-52
 Match length 148
 % identity 61
 NCBI Description (AL109619) putative protein [Arabidopsis thaliana]

Seq. No. 399601
 Seq. ID LIB3431-026-P1-K1-C3
 Method BLASTX
 NCBI GI g132105
 BLAST score 713
 E value 2.0e-75
 Match length 131
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone POSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 399602
 Seq. ID LIB3431-026-P1-K1-C4
 Method BLASTX
 NCBI GI g125580
 BLAST score 498
 E value 2.0e-50
 Match length 116
 % identity 85
 NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

00684015.101000

>gi_871510_emb_CAA90080_ (Z49900) small GTP-binding protein
[Pisum sativum]

Seq. No. 399608
Seq. ID LIB3431-026-P1-K1-D10
Method BLASTX
NCBI GI g115787
BLAST score 489
E value 2.0e-49
Match length 113
% identity 87
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 399609
Seq. ID LIB3431-026-P1-K1-D11
Method BLASTX
NCBI GI g2688839
BLAST score 531
E value 3.0e-54
Match length 136
% identity 69
NCBI Description (AF003347) ATP phosphoribosyltransferase [Thlaspi
goesingense]

Seq. No. 399610
Seq. ID LIB3431-026-P1-K1-D12
Method BLASTX
NCBI GI g3176690
BLAST score 639
E value 6.0e-67
Match length 129
% identity 91
NCBI Description (AC003671) Similar to ubiquitin ligase gb_D63905 from S.
cerevisiae. EST gb_R65295 comes from this gene.
[Arabidopsis thaliana]

Seq. No. 399611
Seq. ID LIB3431-026-P1-K1-D4
Method BLASTX
NCBI GI g3004565
BLAST score 289
E value 8.0e-29
Match length 80
% identity 79
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 399612
Seq. ID LIB3431-026-P1-K1-D5
Method BLASTX
NCBI GI g320618
BLAST score 558
E value 2.0e-57
Match length 124

000101015-101000

% identity 85
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 399613
 Seq. ID LIB3431-026-P1-K1-D6
 Method BLASTX
 NCBI GI g733458
 BLAST score 145
 E value 4.0e-09
 Match length 77
 % identity 51
 NCBI Description (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
 [Zea mays]

Seq. No. 399614
 Seq. ID LIB3431-026-P1-K1-D8
 Method BLASTX
 NCBI GI g170131
 BLAST score 391
 E value 8.0e-38
 Match length 116
 % identity 65
 NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 399615
 Seq. ID LIB3431-026-P1-K1-D9
 Method BLASTX
 NCBI GI g2570511
 BLAST score 561
 E value 8.0e-58
 Match length 107
 % identity 97
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 399616
 Seq. ID LIB3431-026-P1-K1-E10
 Method BLASTX
 NCBI GI g2673913
 BLAST score 244
 E value 1.0e-20
 Match length 66
 % identity 64
 NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399617
 Seq. ID LIB3431-026-P1-K1-E11
 Method BLASTX
 NCBI GI g2055273
 BLAST score 611
 E value 1.0e-63
 Match length 135
 % identity 87
 NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

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Seq. No.      399627
Seq. ID      LIB3431-026-P1-K1-F7
Method       BLASTX
NCBI GI      g733454
BLAST score   431
E value      1.0e-42
Match length  103
% identity    81
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
```

Seq. No.	399628
Seq. ID	LIB3431-026-P1-K1-F8
Method	BLASTX
NCBI GI	g3859597
BLAST score	275
E value	3.0e-24
Match length	96
% identity	54
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana]

```
Seq. No.      399629
Seq. ID      LIB3431-026-P1-K1-G1
Method       BLASTN
NCBI GI      g1619603
BLAST score   316
E value      1.0e-178
Match length  335
% identity    99
NCBI Description  O.sativa mRNA for lipid transfer protein
                  >gi_1667589_gb_U77295_OSU77295 Oryza sativa lipid transfer
                  protein (LTP) mRNA, complete cds
```

Seq. No.	399630
Seq. ID	LIB3431-026-P1-K1-G10
Method	BLASTX
NCBI GI	g3242708
BLAST score	414
E value	2.0e-40
Match length	144
% identity	56
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

```
Seq. No.      399631
Seq. ID      LIB3431-026-P1-K1-G11
Method       BLASTX
NCBI GI      g2624326
BLAST score   245
E value      8.0e-21
Match length  56
% identity   86
NCBI Description (AJ002893) OsGRP1 [Oryza sativa]
```

```
Seq. No.      399632
Seq. ID      LIB3431-026-P1-K1-G2
Method       BLASTX
```


Method	BLASTX
NCBI GI	g129915
BLAST score	492
E value	8.0e-50
Match length	104
% identity	92
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_66912_pir_TVWTGC phosphoglycerate kinase (EC 2.7.2.3) precursor, chloroplast - wheat >gi_21833_emb_CAA33303 (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum aestivum] >gi_3293043_emb_CAA51931_(X73528) phosphoglycerate kinase [Triticum aestivum]
Seq. No.	399638
Seq. ID	LIB3431-026-P1-K1-G9
Method	BLASTX
NCBI GI	g131176
BLAST score	299
E value	5.0e-27
Match length	58
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir_F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_(Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]
Seq. No.	399639
Seq. ID	LIB3431-026-P1-K1-H11
Method	BLASTX
NCBI GI	g3292814
BLAST score	298
E value	7.0e-27
Match length	80
% identity	68
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	399640
Seq. ID	LIB3431-026-P1-K1-H3
Method	BLASTX
NCBI GI	g3411227
BLAST score	402
E value	3.0e-39
Match length	84
% identity	90
NCBI Description	(AF078874) NBS-LRR type disease resistance protein O2 [Avena sativa]
Seq. No.	399641
Seq. ID	LIB3431-026-P1-K1-H4
Method	BLASTX
NCBI GI	g3913018
BLAST score	694
E value	2.0e-73
Match length	140

% identity	100
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]
Seq. No.	399642
Seq. ID	LIB3431-026-P1-K1-H5
Method	BLASTX
NCBI GI	g5007084
BLAST score	383
E value	3.0e-37
Match length	90
% identity	80
NCBI Description	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]
Seq. No.	399643
Seq. ID	LIB3431-026-P1-K1-H7
Method	BLASTX
NCBI GI	g3176725
BLAST score	200
E value	2.0e-15
Match length	98
% identity	41
NCBI Description	(AC002392) unknown protein [Arabidopsis thaliana]
Seq. No.	399644
Seq. ID	LIB3431-026-P1-K1-H8
Method	BLASTX
NCBI GI	g2754849
BLAST score	248
E value	5.0e-21
Match length	55
% identity	87
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]
Seq. No.	399645
Seq. ID	LIB3431-026-P1-K1-H9
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	1.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]
Seq. No.	399646
Seq. ID	LIB3431-026-P1-N1-A1
Method	BLASTN
NCBI GI	g3777599
BLAST score	44
E value	2.0e-15
Match length	155
% identity	88
NCBI Description	Oryza sativa clone LS101 50S ribosomal protein L5 (rpl5) mRNA, nuclear gene encoding chloroplast protein, partial

```
Seq. No.          399648
Seq. ID           LIB3431-026-P1-N1-A11
Method            BLASTX
NCBI GI           g3345477
BLAST score       226
E value           2.0e-18
Match length      42
% identity         100
NCBI Description  (AB016283) carbonic anhydrase [Oryza sativa]
```

```
Seq. No.          399649
Seq. ID           LIB3431-026-P1-N1-A12
Method            BLASTX
NCBI GI           g421916
BLAST score       167
E value           1.0e-11
Match length      30
% identity        100
NCBI Description   chlorophyll a/b-binding protein - English ivy (fragment)
                   >gi_12582_emb_CAA48410_ (X68333) light harvesting
                   chlorophyll a /b binding protein [Hedera helix]
```

```
Seq. No.          399650
Seq. ID           LIB3431-026-P1-N1-A2
Method            BLASTX
NCBI GI           g671740
BLAST score       345
E value           2.0e-32
Match length      65
% identity         98
NCBI Description   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
```

```
Seq. No.      399651
Seq. ID      LIB3431-026-P1-N1-A3
Method       BLASTX
NCBI GI      g2462750
BLAST score   240
E value      4.0e-20
```

```

Match length      65
% identity        69
NCBI Description  (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]

```

```
Seq. No.      399652
Seq. ID      LIB3431-026-P1-N1-A4
Method       BLASTX
NCBI GI      g132105
BLAST score   277
E value      2.0e-24
Match length  53
% identity    100
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose biphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.      399653
Seq. ID       LIB3431-026-P1-N1-A5
Method        BLASTX
NCBI GI       g3345477
BLAST score    210
E value       1.0e-16
Match length   40
% identity     97
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

```
Seq. No.      399654
Seq. ID       LIB3431-026-P1-N1-A6
Method        BLASTX
NCBI GI       g4538920
BLAST score    226
E value       2.0e-18
Match length   59
% identity     81
NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis thaliana]
```

```
Seq. No.      399655
Seq. ID      LIB3431-026-P1-N1-A7
Method       BLASTX
NCBI GI      g3913437
BLAST score   196
E value      2.0e-15
Match length  41
% identity    85
NCBI Description  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
                HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
                [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)
                RNA helicase [Arabidopsis thaliana]
```

```
Seq. No.      299656
Seq. ID      LIB3431-026-P1-N1-A8
Method       BLASTX
NCBI GI      g132105
BLAST score   301
E value      3.0e-27
Match length  57
% identity    100
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphtosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.          399657
Seq. ID           LIB3431-026-P1-N1-A9
Method            BLASTN
NCBI GI           g2305114
BLAST score       295
E value           1.0e-165
Match length      390
% identity        94
NCBI Description   Oryza sativa ferredoxin mRNA, complete cds
```

```
Seq. No.      399658
Seq. ID       LIB3431-026-P1-N1-B1
Method        BLASTN
NCBI GI       g5360229
BLAST score    393
E value        0.0e+00
Match length   393
% identity     100
NCBI Description  Oryza sativa mRNA for Ran, complete cds
```

```
Seq. No.          399659
Seq. ID           LIB3431-026-P1-N1-B10
Method            BLASTX
NCBI GI           g1617197
BLAST score       230
E value           5.0e-19
Match length      49
% identity         86
NCBI Description   (Z72488) CP12 [Nicotiana tabacum]
```

```
Seq. No.      399660
Seq. ID       LIB3431-026-P1-N1-B12
Method        BLASTX
NCBI GI       g4588906
BLAST score   465
E value       2.0e-46
Match length  100
% identity    88
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]
```

000T0T" 9T04B960

Seq. No. 399661
Seq. ID LIB3431-026-P1-N1-B2
Method BLASTN
NCBI GI g5478796
BLAST score 349
E value 0.0e+00
Match length 431
% identity 100
NCBI Description Oryza sativa CAO mRNA for chlorophyll b synthase, partial cds

Seq. No. 399662
Seq. ID LIB3431-026-P1-N1-B3
Method BLASTX
NCBI GI g1173347
BLAST score 250
E value 2.0e-21
Match length 54
% identity 94
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507 (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 399663
Seq. ID LIB3431-026-P1-N1-B4
Method BLASTX
NCBI GI g1835731
BLAST score 359
E value 4.0e-34
Match length 80
% identity 88
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399664
Seq. ID LIB3431-026-P1-N1-B5
Method BLASTX
NCBI GI g1835731
BLAST score 359
E value 4.0e-34
Match length 80
% identity 88
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399665
Seq. ID LIB3431-026-P1-N1-B6
Method BLASTX
NCBI GI g3929924
BLAST score 292
E value 3.0e-26
Match length 56
% identity 98
NCBI Description (AB020502) catalase [Oryza sativa]

[Phalaenopsis sp. 'KCbutterfly']

Seq. No. 399676
Seq. ID LIB3431-026-P1-N1-D3
Method BLASTX
NCBI GI g120661
BLAST score 181
E value 3.0e-13
Match length 45
% identity 76
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 399677
Seq. ID LIB3431-026-P1-N1-D4
Method BLASTX
NCBI GI g3004565
BLAST score 337
E value 2.0e-31
Match length 94
% identity 67
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 399678
Seq. ID LIB3431-026-P1-N1-D5
Method BLASTX
NCBI GI g115787
BLAST score 409
E value 6.0e-40
Match length 77
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 399679
Seq. ID LIB3431-026-P1-N1-D6
Method BLASTX
NCBI GI g543939
BLAST score 160
E value 9.0e-11
Match length 39
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR
>gi_541819_pir_S40210 chlorophyll a/b-binding protein CP24
precursor - spinach >gi_437991_emb_CAA81105.1 (Z25886) 20
kDa protein of CP24 precursor protein [Spinacia oleracea]

Seq. No. 399680
Seq. ID LIB3431-026-P1-N1-D8
Method BLASTX
NCBI GI g170131
BLAST score 218
E value 1.0e-17

09684015 "101000

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 399686
Seq. ID LIB3431-026-P1-N1-E7
Method BLASTX
NCBI GI g1617197
BLAST score 164
E value 3.0e-11
Match length 33
% identity 88

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399687
Seq. ID LIB3431-026-P1-N1-E8
Method BLASTX
NCBI GI g2754849
BLAST score 186
E value 8.0e-14
Match length 45
% identity 80

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No. 399688
Seq. ID LIB3431-026-P1-N1-F11
Method BLASTX
NCBI GI g3126854
BLAST score 431
E value 1.0e-42
Match length 82
% identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 399689
Seq. ID LIB3431-026-P1-N1-F12
Method BLASTX
NCBI GI g482311
BLAST score 508
E value 1.0e-51
Match length 99
% identity 100

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 399690
Seq. ID LIB3431-026-P1-N1-F2
Method BLASTX
NCBI GI g132105
BLAST score 301
E value 2.0e-27
Match length 57
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

Figure 6

```
Seq. No.          399701
Seq. ID           LIB3431-026-P1-N1-G9
Method            BLASTX
NCBI GI           g1311176
BLAST score       187
E value           6.0e-14
Match length      37
% identity        97
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
                  (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                  >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
                  barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
                  -46 to 101) [Hordeum_vulgare] >gi_226163_prf_1413233A
                  10.8kd photosystem I protein [Hordeum vulgare var.
                  distichum]
```

```
Seq. No.      399702
Seq. ID       LIB3431-026-P1-N1-H11
Method        BLASTX
NCBI GI       g3292814
BLAST score   232
E value       3.0e-19
Match length  57
% identity    72
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      399703
Seq. ID       LIB3431-026-P1-N1-H3
Method        BLASTX
NCBI GI       g4490715
BLAST score   147
E value       3.0e-09
Match length  99
% identity    34
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          399704
Seq. ID           LIB3431-026-P1-N1-H4
Method            BLASTX
NCBI GI           g3913018
BLAST score       166
E value           2.0e-11
Match length      33
% identity        100
```


05084016 101000

[illegible]

Seq. No.	399728
Seq. ID	LIB3431-027-P1-K1-C12
Method	BLASTX
NCBI GI	g100796
BLAST score	752
E value	4.0e-80
Match length	152
% identity	94
NCBI Description	phosphoribulokinase (EC 2.7.1.19) - wheat

51136

Match length 118
 % identity 68
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 399730
 Seq. ID LIB3431-027-P1-K1-C4
 Method BLASTX
 NCBI GI g1669341
 BLAST score 219
 E value 1.0e-17
 Match length 133
 % identity 41
 NCBI Description (D45066) AOBP (ascorbate oxidase promoter-binding protein)
 [Cucurbita maxima]

Seq. No. 399731
 Seq. ID LIB3431-027-P1-K1-C5
 Method BLASTX
 NCBI GI g4585882
 BLAST score 498
 E value 2.0e-50
 Match length 150
 % identity 64
 NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
 [Arabidopsis thaliana]

Seq. No. 399732
 Seq. ID LIB3431-027-P1-K1-C6
 Method BLASTX
 NCBI GI g5922612
 BLAST score 282
 E value 5.0e-25
 Match length 127
 % identity 46
 NCBI Description (AP000492) EST AU078118(E3904) corresponds to a region of
 the predicted gene.; similar to Arabidopsis thaliana BAC
 IG002P16; No definition line found. (AF007270) [Oryza
 sativa]

Seq. No. 399733
 Seq. ID LIB3431-027-P1-K1-C9
 Method BLASTX
 NCBI GI g671740
 BLAST score 219
 E value 1.0e-17
 Match length 48
 % identity 88
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 399734
 Seq. ID LIB3431-027-P1-K1-D1
 Method BLASTX
 NCBI GI g2244926
 BLAST score 292


```
Seq. No.      399745
Seq. ID      LIB3431-027-P1-K1-E6
Method       BLASTX
NCBI GI      g5354158
BLAST score   384
E value      3.0e-43
Match length  140
% identity    64
NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis
thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842)
digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
>gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918)
digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
```

```
Seq. No.      399746
Seq. ID      LIB3431-027-P1-K1-E7
Method       BLASTX
NCBI GI      g729668
BLAST score   241
E value      3.0e-20
Match length  68
% identity    63
NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1,
                drought-inducible - Lycopersicon pennellii >gi_436823
                (U01890). Solanum pennellii histone H1 [Solanum pennellii]
```

```
Seq. No.      399747
Seq. ID      LIB3431-027-P1-K1-E8
Method       BLASTX
NCBI GI      g1835731
BLAST score   412
E value      3.0e-40
Match length  89
% identity    88
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

```
Seq. No.      399748
Seq. ID       LIB3431-027-P1-K1-E9
Method        BLASTX
NCBI GI       g3885894
BLAST score    464
E value       2.0e-46
Match length   110
% identity     82
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
```

Seq. No.	399749
Seq. ID	LIB3431-027-P1-K1-F1
Method	BLASTX
NCBI GI	g1076722
BLAST score	667
E value	4.0e-70
Match length	144
% identity	90
NCBI Description	hypothetical protein - barley (fragment)

```
Seq. No.      399750
Seq. ID      LIB3431-027-P1-K1-F10
Method       BLASTX
NCBI GI      g1777961
BLAST score   504
E value      5.0e-51
Match length  154
% identity    58
NCBI Description (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum
vulgare]
```

```
Seq. No.      399751
Seq. ID      LIB3431-027-P1-K1-F11
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      9.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

```
Seq. No.      399752
Seq. ID      LIB3431-027-P1-K1-F12
Method       BLASTX
NCBI GI      g3510256
BLAST score   157
E value      2.0e-10
Match length  106
% identity    32
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      399753
Seq. ID      LIB3431-027-P1-K1-F2
Method       BLASTX
NCBI GI      g3204108
BLAST score   570
E value      8.0e-59
Match length  118
% identity    87
NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer
arietinum]
```

```
Seq. No.      399754
Seq. ID      LIB3431-027-P1-K1-F3
Method       BLASTX
NCBI GI      g132105
BLAST score   666
E value      5.0e-70
Match length  142
% identity    89
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
```

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 399755
 Seq. ID LIB3431-027-P1-K1-F4
 Method BLASTX
 NCBI GI g3789952
 BLAST score 307
 E value 6.0e-28
 Match length 66
 % identity 88
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 399756
 Seq. ID LIB3431-027-P1-K1-F5
 Method BLASTX
 NCBI GI g1076800
 BLAST score 717
 E value 5.0e-76
 Match length 155
 % identity 87
 NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
 maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
 peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate
 peroxidase [Zea mays]

Seq. No. 399757
 Seq. ID LIB3431-027-P1-K1-F6
 Method BLASTX
 NCBI GI g1835731
 BLAST score 531
 E value 3.0e-54
 Match length 101
 % identity 100
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399758
 Seq. ID LIB3431-027-P1-K1-F8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 671
 E value 1.0e-70
 Match length 126
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 399759
 Seq. ID LIB3431-027-P1-K1-F9
 Method BLASTX
 NCBI GI g6066383
 BLAST score 236
 E value 5.0e-20
 Match length 49
 % identity 98

000001-9101000

NCBI GI g5103831
 BLAST score 281
 E value 5.0e-25
 Match length 94
 % identity 60
 NCBI Description (AC007591) ESTs gb_H37032, gb_R6425, gb_Z34651, gb_N37268, gb_AA713172 and gb_Z34241 come from this gene. [Arabidopsis thaliana]

Seq. No. 399766
 Seq. ID LIB3431-027-P1-K1-G6
 Method BLASTN
 NCBI GI g3075487
 BLAST score 157
 E value 5.0e-83
 Match length 157
 % identity 100
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 399767
 Seq. ID LIB3431-027-P1-K1-G7
 Method BLASTX
 NCBI GI g5815133
 BLAST score 183
 E value 2.0e-13
 Match length 99
 % identity 37
 NCBI Description (AF169386) SPO11 [Mus musculus]

Seq. No. 399768
 Seq. ID LIB3431-027-P1-K1-G8
 Method BLASTX
 NCBI GI g3763918
 BLAST score 236
 E value 1.0e-19
 Match length 67
 % identity 70
 NCBI Description (AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No. 399769
 Seq. ID LIB3431-027-P1-K1-H1
 Method BLASTX
 NCBI GI g1169544
 BLAST score 540
 E value 3.0e-55
 Match length 154
 % identity 67
 NCBI Description ERD1 PROTEIN PRECURSOR >gi_541859_pir_JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) ERD1 protein [Arabidopsis thaliana]

Seq. No. 399770
 Seq. ID LIB3431-027-P1-K1-H11
 Method BLASTX
 NCBI GI g3075488

```
BLAST score      572
E value         1.0e-65
Match length    139
% identity      91
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
```

```
Seq. No.      399771
Seq. ID      LIB3431-027-P1-K1-H12
Method       BLASTX
NCBI GI      g3789954
BLAST score   148
E value      2.0e-19
Match length  118
% identity    53
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]
```

```
Seq. No.      399772
Seq. ID      LIB3431-027-P1-K1-H3
Method       BLASTX
NCBI GI      g4587571
BLAST score   425
E value      8.0e-42
Match length  104
% identity    75
NCBI Description (AC006550) Belongs to the PF_01027 Uncharacterized protein
family UPF0005 with 7 transmembrane domains. [Arabidopsis
thaliana]
```

```
Seq. No.      399773
Seq. ID      LIB3431-027-P1-K1-H5
Method       BLASTX
NCBI GI      g115796
BLAST score   721
E value      2.0e-76
Match length  138
% identity    98
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
                  CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
```

```
Seq. No.      399774
Seq. ID      LIB3431-027-P1-K1-H6
Method       BLASTX
NCBI GI      g3789954
BLAST score   186
E value      2.0e-14
Match length  64
% identity    61
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]
```

```
Seq. No.      399775
Seq. ID       LIB3431-027-P1-K1-H7
Method        BLASTX
NCBI GI       q3881189
```

```

BLAST score      489
E value          3.0e-49
Match length     144
% identity       61
NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337
                  comes from this gene; cDNA EST EMBL:C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y

```

```
Seq. No.      399776
Seq. ID      LIB3431-027-P1-K1-H8
Method       BLASTX
NCBI GI      g320618
BLAST score   489
E value      2.0e-49
Match length  109
% identity    85
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]
```

```
Seq. No.      399777
Seq. ID       LIB3431-027-P1-K1-H9
Method        BLASTX
NCBI GI       g482311
BLAST score    731
E value        1.0e-77
Match length   142
% identity     100
NCBI Description  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
```

```
Seq. No.      399778
Seq. ID      LIB3431-027-P1-N1-A1
Method       BLASTX
NCBI GI      g687677
BLAST score   230
E value      4.0e-19
Match length  51
% identity    86
NCBI Description (U19925) unknown [Arabidopsis thaliana]
```

Seq. No.	399779
Seq. ID	LIB3431-027-P1-N1-A11
Method	BLASTX
NCBI GI	g3413423
BLAST score	169
E value	7.0e-12
Match length	64
% identity	48
NCBI Description	(AJ006309) hypothetical protein [Arabidopsis thaliana]

Seq. No.	399780
Seq. ID	LIB3431-027-P1-N1-A12

Seq. No.	399785
Seq. ID	LIB3431-027-P1-N1-A8
Method	BLASTX
NCBI GI	g733454
BLAST score	271
E value	8.0e-24
Match length	56
% identity	95
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]
Seq. No.	399786
Seq. ID	LIB3431-027-P1-N1-A9
Method	BLASTX
NCBI GI	g3885892
BLAST score	338
E value	1.0e-31
Match length	65
% identity	100
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.	399787
Seq. ID	LIB3431-027-P1-N1-B1
Method	BLASTX
NCBI GI	g482311
BLAST score	186
E value	6.0e-14
Match length	36
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	399788
Seq. ID	LIB3431-027-P1-N1-B10
Method	BLASTN
NCBI GI	g169798
BLAST score	42
E value	3.0e-14
Match length	94
% identity	86
NCBI Description	Oryza sativa 16.9 kDa heat shock protein gene, complete cds
Seq. No.	399789
Seq. ID	LIB3431-027-P1-N1-B2
Method	BLASTX
NCBI GI	g482311
BLAST score	154
E value	4.0e-10
Match length	44
% identity	73
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	399790
Seq. ID	LIB3431-027-P1-N1-B3

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 399799
Seq. ID LIB3431-027-P1-N1-C8
Method BLASTX
NCBI GI g6063542
BLAST score 225
E value 2.0e-18
Match length 41
% identity 98
NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 399800
Seq. ID LIB3431-027-P1-N1-C9
Method BLASTN
NCBI GI g218209
BLAST score 41
E value 1.0e-13
Match length 131
% identity 81
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 399801
Seq. ID LIB3431-027-P1-N1-D1
Method BLASTX
NCBI GI g2244926
BLAST score 292
E value 3.0e-26
Match length 88
% identity 65
NCBI Description (Z97339) glutaredoxin homolog [Arabidopsis thaliana]

Seq. No. 399802
Seq. ID LIB3431-027-P1-N1-D10
Method BLASTX
NCBI GI g4115337
BLAST score 201
E value 1.0e-15
Match length 41
% identity 16
NCBI Description (L81141) ubiquitin [Pisum sativum]

Seq. No. 399803
Seq. ID LIB3431-027-P1-N1-D12
Method BLASTX
NCBI GI g1617197
BLAST score 212
E value 6.0e-17
Match length 44
% identity 89
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399804

```
Seq. ID      LIB3431-027-P1-N1-D2
Method       BLASTX
NCBI GI      g1076724
BLAST score   284
E value      2.0e-25
Match length  56
% identity    95
NCBI Description LHCI-680, photosystem I antenna protein - barley
               >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
               antenna protein [Hordeum vulgare]
```

```
Seq. No.          399805
Seq. ID          LIB3431-027-P1-N1-D4
Method           BLASTX
NCBI GI          g548605
BLAST score      484
E value          1.0e-48
Match length     126
% identity       79
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

```
Seq. No.      399806
Seq. ID      LIB3431-027-P1-N1-D7
Method       BLASTX
NCBI GI      g3036951
BLAST score   343
E value      2.0e-32
Match length  65
% identity    100
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
[Nicotiana sylvestris]
```

```
Seq. No.      399807
Seq. ID      LIB3431-027-P1-N1-D8
Method       BLASTX
NCBI GI      g421916
BLAST score   243
E value      1.0e-20
Match length  45
% identity    100
NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
                >gi_12582_emb_CAA48410_ (X68333) light harvesting
                chlorophyll a /b binding protein [Hedera helix]
```

```
Seq. No.      399808
Seq. ID      LIB3431-027-P1-N1-E1
Method       BLASTN
NCBI GI      g2570510
BLAST score   150
E value      8.0e-79
Match length  226
% identity    92
NCBI Description  Oryza sativa chlorophyll a-b binding protein mRNA, complete
```

09084016 101000

```
Seq. No.      399810
Seq. ID      LIB3431-027-P1-N1-E12
Method       BLASTX
NCBI GI      g132105
BLAST score   169
E value      2.0e-20
Match length  55
% identity   98
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.          399811
Seq. ID           LIB3431-027-P1-N1-E4
Method            BLASTN
NCBI GI           g2570514
BLAST score       266
E value           1.0e-148
Match length      369
% identity        98
NCBI Description   Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
```

```
Seq. No.          399812
Seq. ID           LIB3431-027-P1-N1-E5
Method            BLASTX
NCBI GI           g451193
BLAST score       284
E value           2.0e-25
Match length      87
% identity        66
NCBI Description  (L28008) wali7 [Triticum aestivum]
                  >qi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
```

```
Seq. No.      399813
Seq. ID       LIB3431-027-P1-N1-E6
Method        BLASTX
NCBI GI       g5354158
BLAST score    155
E value       3.0e-10
```

Match length 42
 % identity 60
 NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No. 399814
 Seq. ID LIB3431-027-P1-N1-E8
 Method BLASTX
 NCBI GI g1835731
 BLAST score 359
 E value 4.0e-34
 Match length 80
 % identity 88
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399815
 Seq. ID LIB3431-027-P1-N1-E9
 Method BLASTX
 NCBI GI g3885894
 BLAST score 398
 E value 1.0e-38
 Match length 90
 % identity 86
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 399816
 Seq. ID LIB3431-027-P1-N1-F1
 Method BLASTX
 NCBI GI g3328221
 BLAST score 348
 E value 7.0e-33
 Match length 69
 % identity 93
 NCBI Description (AF076920) thioredoxin peroxidase [Secale cereale]

Seq. No. 399817
 Seq. ID LIB3431-027-P1-N1-F10
 Method BLASTX
 NCBI GI g2826842
 BLAST score 268
 E value 2.0e-23
 Match length 75
 % identity 63
 NCBI Description (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]

Seq. No. 399818
 Seq. ID LIB3431-027-P1-N1-F11
 Method BLASTN
 NCBI GI g2072554
 BLAST score 361
 E value 0.0e+00
 Match length 389
 % identity 98
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

[illegible]

```
Seq. No.      399820
Seq. ID      LIB3431-027-P1-N1-F3
Method       BLASTN
NCBI GI      g218207
BLAST score   195
E value      1.0e-105
Match length  315
% identity    90
NCBI Description  Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
poSSS1139
```

```
Seq. No.          399821
Seq. ID           LIB3431-027-P1-N1-F4
Method            BLASTN
NCBI GI           g3789951
BLAST score       134
E value           4.0e-69
Match length      318
% identity        86
NCBI Description   Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
```

```
Seq. No.      399822
Seq. ID       LIB3431-027-P1-N1-F5
Method        BLASTN
NCBI GI       g433216
BLAST score    223
E value        1.0e-122
Match length   232
% identity     99
NCBI Description  Rice mRNA for ascorbate peroxidase (gene name SS622),
                  partial cds
```

```
Seq. No.      399823
Seq. ID      LIB3431-027-P1-N1-F6
Method       BLASTX
NCBI GI      g1835731
BLAST score   326
E value      3.0e-30
Match length  73
% identity    86
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```


NCBI Description (AJ010449) glutathione transferase [*Alopecurus myosuroides*]

Seq. No. 399845
 Seq. ID LIB3431-028-P1-K1-A9
 Method BLASTX
 NCBI GI g1698548
 BLAST score 456
 E value 2.0e-45
 Match length 137
 % identity 60
 NCBI Description (U58971) calmodulin-binding protein [*Nicotiana tabacum*]

Seq. No. 399846
 Seq. ID LIB3431-028-P1-K1-B1
 Method BLASTX
 NCBI GI g3345477
 BLAST score 147
 E value 3.0e-09
 Match length 28
 % identity 100
 NCBI Description (AB016283) carbonic anhydrase [*Oryza sativa*]

Seq. No. 399847
 Seq. ID LIB3431-028-P1-K1-B10
 Method BLASTX
 NCBI GI g5921189
 BLAST score 364
 E value 1.0e-34
 Match length 153
 % identity 49
 NCBI Description CYTOCHROME P450 71C4 >gi_550542_emb_CAA57425_ (X81831)
 cytochrome P450 [*Zea mays*] >gi_1850903_emb_CAA72196_
 (Y11368) cytochrome p450 [*Zea mays*]

Seq. No. 399848
 Seq. ID LIB3431-028-P1-K1-B12
 Method BLASTX
 NCBI GI g320618
 BLAST score 408
 E value 7.0e-40
 Match length 98
 % identity 81
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [*Oryza sativa*]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [*Oryza sativa*]

Seq. No. 399849
 Seq. ID LIB3431-028-P1-K1-B2
 Method BLASTX
 NCBI GI g6002102
 BLAST score 322
 E value 1.0e-29
 Match length 91
 % identity 68
 NCBI Description (AJ249833) Acyl-CoA binding protein (ACBP) [*Digitalis*]

[illegible]

```
Seq. No.          399851
Seq. ID          LIB3431-028-P1-K1-B5
Method           BLASTX
NCBI GI          g2499775
BLAST score      188
E value          5.0e-14
Match length     84
% identity       49
NCBI Description  51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL
                  CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) >gi_915280
                  (U16959) FKBP51 [Mus musculus] >gi_1020307 (U36220) FK506
                  binding protein 51 [Mus musculus]
```

Seq. No.	399852
Seq. ID	LIB3431-028-P1-K1-C1
Method	BLASTX
NCBI GI	g5802955
BLAST score	194
E value	8.0e-15
Match length	79
% identity	47
NCBI Description	(AF178990) stress related protein [Vitis riparia]

Seq. No.	399853
Seq. ID	LIB3431-028-P1-K1-C10
Method	BLASTX
NCBI GI	g2734085
BLAST score	154
E value	5.0e-10
Match length	107
% identity	28
NCBI Description	(AF003136) contains similarity to ATP synthase subunit B [Caenorhabditis elegans]

```
Seq. No.          399854
Seq. ID           LIB3431-028-P1-K1-C12
Method            BLASTN
NCBI GI           g6015437
BLAST score       35
E value           6.0e-10
Match length      35
% identity         100
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
```

51161

09684016-101000

[Hordeum vulgare]

Seq. No. 399865
Seq. ID LIB3431-028-P1-K1-D5
Method BLASTN
NCBI GI g3885891
BLAST score 119
E value 2.0e-60
Match length 156
% identity 100
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
mRNA, complete cds

Seq. No. 399866
Seq. ID LIB3431-028-P1-K1-D6
Method BLASTX
NCBI GI g2501189
BLAST score 164
E value 7.0e-12
Match length 33
% identity 91
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
>gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme
[Zea mays]

Seq. No. 399867
Seq. ID LIB3431-028-P1-K1-D7
Method BLASTX
NCBI GI g3341692
BLAST score 324
E value 6.0e-30
Match length 141
% identity 54
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 399868
Seq. ID LIB3431-028-P1-K1-D8
Method BLASTX
NCBI GI g2570511
BLAST score 660
E value 9.0e-72
Match length 138
% identity 97
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 399869
Seq. ID LIB3431-028-P1-K1-D9
Method BLASTX
NCBI GI g1076800
BLAST score 561
E value 1.0e-57
Match length 121
% identity 85
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate

0967-016

```
Seq. No.          399871
Seq. ID          LIB3431-028-P1-K1-E2
Method           BLASTX
NCBI GI          g2633727
BLAST score      148
E value          2.0e-09
Match length     137
% identity       28
NCBI Description  (Z99111) ykrT [Bacillus subtilis]
```

Seq. No.	399873
Seq. ID	LIB3431-028-P1-K1-E4
Method	BLASTX
NCBI GI	g1661160
BLAST score	382
E value	8.0e-37
Match length	89
% identity	80
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

51165

Match length	154
% identity	60
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]
Seq. No.	399875
Seq. ID	LIB3431-028-P1-K1-E6
Method	BLASTN
NCBI GI	g3789953
BLAST score	55
E value	5.0e-22
Match length	77
% identity	92
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	399876
Seq. ID	LIB3431-028-P1-K1-E7
Method	BLASTX
NCBI GI	g3560529
BLAST score	336
E value	2.0e-31
Match length	87
% identity	75
NCBI Description	(AF039598) light harvesting chlorophyll A/B binding protein [Prunus persica]
Seq. No.	399877
Seq. ID	LIB3431-028-P1-K1-E8
Method	BLASTX
NCBI GI	g2407281
BLAST score	349
E value	7.0e-33
Match length	65
% identity	100
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]
Seq. No.	399878
Seq. ID	LIB3431-028-P1-K1-E9
Method	BLASTX
NCBI GI	g3329386
BLAST score	334
E value	4.0e-31
Match length	138
% identity	47
NCBI Description	(AF038958) synaptic glycoprotein SC2 spliced variant [Homo sapiens]
Seq. No.	399879
Seq. ID	LIB3431-028-P1-K1-F10
Method	BLASTX
NCBI GI	g2570511
BLAST score	644
E value	3.0e-67
Match length	136
% identity	95

Seq. No.	399890
Seq. ID	LIB3431-028-P1-K1-G3
Method	BLASTX
NCBI GI	g5902394
BLAST score	155
E value	3.0e-10
Match length	37
% identity	86
NCBI Description	(AC008148) Putative phosphoglucomutase [Arabidopsis thaliana]
Seq. No.	399891
Seq. ID	LIB3431-028-P1-K1-G4
Method	BLASTX
NCBI GI	g3126854
BLAST score	645
E value	1.0e-67
Match length	121
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	399892
Seq. ID	LIB3431-028-P1-K1-G5
Method	BLASTX
NCBI GI	g3668091
BLAST score	519
E value	8.0e-53
Match length	149
% identity	14
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]
Seq. No.	399893
Seq. ID	LIB3431-028-P1-K1-G6
Method	BLASTX
NCBI GI	g2780746
BLAST score	717
E value	5.0e-76
Match length	138
% identity	100
NCBI Description	(AB005290) plastid RNA polymerase sigma factor [Oryza sativa]
Seq. No.	399894
Seq. ID	LIB3431-028-P1-K1-G8
Method	BLASTX
NCBI GI	g710308
BLAST score	699
E value	6.0e-74
Match length	153
% identity	88
NCBI Description	(U11693) victorin binding protein [Avena sativa]
Seq. No.	399895
Seq. ID	LIB3431-028-P1-K1-G9
Method	BLASTX
NCBI GI	g4510406
BLAST score	174

E value 1.0e-12
 Match length 104
 % identity 48
 NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 399896
 Seq. ID LIB3431-028-P1-K1-H1
 Method BLASTX
 NCBI GI g586038
 BLAST score 537
 E value 6.0e-55
 Match length 148
 % identity 72
 NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN, CHLOROPLAST PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC) >gi_480296_pir_S36637 signal recognition particle 54CP protein precursor - Arabidopsis thaliana >gi_396701_emb_CAA79981.1_ (Z21970) 54CP [Arabidopsis thaliana]

Seq. No. 399897
 Seq. ID LIB3431-028-P1-K1-H10
 Method BLASTX
 NCBI GI g132105
 BLAST score 609
 E value 2.0e-63
 Match length 131
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399898
 Seq. ID LIB3431-028-P1-K1-H11
 Method BLASTX
 NCBI GI g1170606
 BLAST score 314
 E value 8.0e-29
 Match length 81
 % identity 77
 NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir_S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No. 399899
 Seq. ID LIB3431-028-P1-K1-H12

Match length 418
 % identity 100
 NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No. 399910
 Seq. ID LIB3431-028-P1-N1-A11
 Method BLASTX
 NCBI GI g2462750
 BLAST score 173
 E value 2.0e-12
 Match length 51
 % identity 67
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 399911
 Seq. ID LIB3431-028-P1-N1-A12
 Method BLASTX
 NCBI GI g3643602
 BLAST score 246
 E value 7.0e-21
 Match length 78
 % identity 58
 NCBI Description (AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No. 399912
 Seq. ID LIB3431-028-P1-N1-A4
 Method BLASTX
 NCBI GI g3808101
 BLAST score 344
 E value 2.0e-32
 Match length 79
 % identity 90
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 399913
 Seq. ID LIB3431-028-P1-N1-A6
 Method BLASTX
 NCBI GI g1835731
 BLAST score 286
 E value 1.0e-25
 Match length 65
 % identity 85
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399914
 Seq. ID LIB3431-028-P1-N1-B1
 Method BLASTX
 NCBI GI g3345477
 BLAST score 277
 E value 1.0e-24
 Match length 52
 % identity 100
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

0001016-101000

Seq. No. 399915
 Seq. ID LIB3431-028-P1-N1-B12
 Method BLASTX
 NCBI GI g289920
 BLAST score 298
 E value 5.0e-27
 Match length 58
 % identity 98
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
 hirsutum]

Seq. No. 399916
 Seq. ID LIB3431-028-P1-N1-B2
 Method BLASTX
 NCBI GI g6002102
 BLAST score 213
 E value 3.0e-17
 Match length 47
 % identity 83
 NCBI Description (AJ249833) Acyl-CoA binding protein (ACBP) [Digitalis
 lanata]

Seq. No. 399917
 Seq. ID LIB3431-028-P1-N1-B3
 Method BLASTN
 NCBI GI g20262
 BLAST score 343
 E value 0.0e+00
 Match length 363
 % identity 99
 NCBI Description O.sativa light-induced mRNA

Seq. No. 399918
 Seq. ID LIB3431-028-P1-N1-B4
 Method BLASTX
 NCBI GI g131176
 BLAST score 275
 E value 2.0e-24
 Match length 57
 % identity 93
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
 (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
 >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
 barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
 -46 to 101) [Hordeum_vulgare] >gi_226163_prf_1413233A
 10.8kD photosystem I protein [Hordeum vulgare var.
 distichum]

Seq. No. 399919
 Seq. ID LIB3431-028-P1-N1-C10
 Method BLASTX
 NCBI GI g1136416
 BLAST score 144
 E value 7.0e-09
 Match length 51
 % identity 57
 NCBI Description (D80000) similar to mitosis-specific chromosome segregation

0966-019-30200

Seq. No.	399924
Seq. ID	LIB3431-028-P1-N1-C8
Method	BLASTX

Method BLASTX
 NCBI GI g3885892
 BLAST score 261
 E value 1.0e-22
 Match length 53
 % identity 98
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 399930
 Seq. ID LIB3431-028-P1-N1-D6
 Method BLASTX
 NCBI GI g2501190
 BLAST score 198
 E value 3.0e-15
 Match length 57
 % identity 74
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 399931
 Seq. ID LIB3431-028-P1-N1-D8
 Method BLASTX
 NCBI GI g115793
 BLAST score 396
 E value 2.0e-38
 Match length 78
 % identity 95
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
 (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein
 type III precursor - barley >gi_19023_emb_CAA44881
 (X63197) type III LHCII CAB precursor protein [Hordeum
 vulgare]

Seq. No. 399932
 Seq. ID LIB3431-028-P1-N1-D9
 Method BLASTN
 NCBI GI g433216
 BLAST score 165
 E value 9.0e-88
 Match length 171
 % identity 99
 NCBI Description Rice mRNA for ascorbate peroxidase (gene name SS622),
 partial cds

Seq. No. 399933
 Seq. ID LIB3431-028-P1-N1-E1
 Method BLASTX
 NCBI GI g132105
 BLAST score 301
 E value 2.0e-27
 Match length 57
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 399934
Seq. ID LIB3431-028-P1-N1-E3
Method BLASTX
NCBI GI g2499417
BLAST score 323
E value 5.0e-30
Match length 74
% identity 82
NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
>gi_1085826_pir_S49248 H-protein - Flaveria anomala
>gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
anomala]

Seq. No. 399935
Seq. ID LIB3431-028-P1-N1-E4
Method BLASTX
NCBI GI g289920
BLAST score 315
E value 5.0e-29
Match length 64
% identity 95
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
hirsutum]

Seq. No. 399936
Seq. ID LIB3431-028-P1-N1-E5
Method BLASTX
NCBI GI g2129703
BLAST score 189
E value 3.0e-14
Match length 87
% identity 49
NCBI Description receptor kinase - Arabidopsis thaliana
>gi_2129704_pir_S71184 receptor kinase - Arabidopsis
thaliana >gi_166692 (M80238) receptor kinase [Arabidopsis
thaliana] >gi_445123_prf_1908429A receptor kinase
[Arabidopsis thaliana]

Seq. No. 399937
Seq. ID LIB3431-028-P1-N1-E6
Method BLASTX
NCBI GI g3789954
BLAST score 357
E value 7.0e-34
Match length 66
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]

Seq. No. 399938

Seq. ID LIB3431-028-P1-N1-E7
 Method BLASTN
 NCBI GI g3126853
 BLAST score 171
 E value 3.0e-91
 Match length 209
 % identity 100
 NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)
 mRNA, nuclear gene encoding chloroplast protein, complete
 cds

Seq. No. 399939
 Seq. ID LIB3431-028-P1-N1-E8
 Method BLASTN
 NCBI GI g218209
 BLAST score 149
 E value 4.0e-78
 Match length 313
 % identity 97
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS2106

Seq. No. 399940
 Seq. ID LIB3431-028-P1-N1-F10
 Method BLASTX
 NCBI GI g115794
 BLAST score 611
 E value 2.0e-63
 Match length 127
 % identity 91
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
 III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
 protein type III precursor (cab-13) - tomato
 >gi_19277_emb_CAA42818_ (X60275) LHCII type III
 [Lycopersicon esculentum]

Seq. No. 399941
 Seq. ID LIB3431-028-P1-N1-F11
 Method BLASTX
 NCBI GI g132105
 BLAST score 406
 E value 1.0e-39
 Match length 76
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 399942
 Seq. ID LIB3431-028-P1-N1-F3

Method BLASTX
NCBI GI g5442410
BLAST score 182
E value 2.0e-13
Match length 78
% identity 50
NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 399943
Seq. ID LIB3431-028-P1-N1-F5
Method BLASTX
NCBI GI g548603
BLAST score 158
E value 1.0e-10
Match length 34
% identity 91
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
>gi_478404_pir_JQ2247 photosystem I chain D precursor -
barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 399944
Seq. ID LIB3431-028-P1-N1-F8
Method BLASTX
NCBI GI g3033382
BLAST score 359
E value 3.0e-34
Match length 76
% identity 86
NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 399945
Seq. ID LIB3431-028-P1-N1-F9
Method BLASTX
NCBI GI g1076724
BLAST score 374
E value 7.0e-36
Match length 72
% identity 94
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 399946
Seq. ID LIB3431-028-P1-N1-G10
Method BLASTX
NCBI GI g120661
BLAST score 180
E value 4.0e-13
Match length 38
% identity 87
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 399947
Seq. ID LIB3431-028-P1-N1-G12

```
Method          BLASTX
NCBI GI         g2072555
BLAST score     231
E value         5.0e-19
Match length    44
% identity      98
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

```
Seq. No.      399948
Seq. ID      LIB3431-028-P1-N1-G2
Method       BLASTN
NCBI GI      g2331130
BLAST score   247
E value      1.0e-136
Match length  275
% identity    97
NCBI Description  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds
```

```
Seq. No.      399949
Seq. ID      LIB3431-028-P1-N1-G3
Method       BLASTX
NCBI GI      g534982
BLAST score   340
E value      6.0e-32
Match length  100
% identity   68
NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]
```

```
Seq. No.      399950
Seq. ID      LIB3431-028-P1-N1-G4
Method       BLASTX
NCBI GI      g3126854
BLAST score   370
E value      2.0e-35
Match length  70
% identity   100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

Seq. No.	399951
Seq. ID	LIB3431-028-P1-N1-G5
Method	BLASTN
NCBI GI	g4680488
BLAST score	45
E value	5.0e-16
Match length	114
% identity	84
NCBI Description	Oryza sativa BAC clone 1.H19, complete sequence

```
Seq. No.      399952
Seq. ID      LIB3431-028-P1-N1-G6
Method       BLASTX
NCBI GI      g2780746
BLAST score   279
E value      8.0e-25
```



```

Seq. No.          399963
Seq. ID           LIB3431-029-P1-K1-A1
Method            BLASTN
NCBI GI           g2570516
BLAST score       55
E value           2.0e-22
Match length      125
% identity        87
NCBI Description   Oryza sativa thioredoxin F isoform mRNA, complete cds

Seq. No.          399964
Seq. ID           LIB3431-029-P1-K1-A10
Method            BLASTX
NCBI GI           g2982362
BLAST score       444
E value           4.0e-44
Match length      91
% identity        89
NCBI Description   (AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.          399965
Seq. ID           LIB3431-029-P1-K1-A11
Method            BLASTN
NCBI GI           g473980
BLAST score       74
E value           1.0e-33
Match length      115
% identity        90
NCBI Description   Rice mRNA, partial homologous to glycine-rich protein gene

Seq. No.          399966
Seq. ID           LIB3431-029-P1-K1-A5
Method            BLASTX
NCBI GI           g2501189
BLAST score       383
E value           6.0e-37
Match length      111
% identity        69
NCBI Description   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
>gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme
[Zea mays]

Seq. No.          399967
Seq. ID           LIB3431-029-P1-K1-A8
Method            BLASTX
NCBI GI           g3075488
BLAST score       270
E value           2.0e-47
Match length      117
% identity        82
NCBI Description   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.          399968
Seq. ID           LIB3431-029-P1-K1-B1
Method            BLASTX

```


Seq. No. 399978
 Seq. ID LIB3431-029-P1-K1-C9
 Method BLASTX
 NCBI GI g2708741
 BLAST score 391
 E value 6.0e-38
 Match length 122
 % identity 61
 NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399979
 Seq. ID LIB3431-029-P1-K1-D10
 Method BLASTX
 NCBI GI g5923674
 BLAST score 468
 E value 7.0e-47
 Match length 135
 % identity 65
 NCBI Description (AC009326) unknown protein [Arabidopsis thaliana]

Seq. No. 399980
 Seq. ID LIB3431-029-P1-K1-D12
 Method BLASTN
 NCBI GI g6063530
 BLAST score 310
 E value 1.0e-174
 Match length 321
 % identity 99
 NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No. 399981
 Seq. ID LIB3431-029-P1-K1-D2
 Method BLASTX
 NCBI GI g464986
 BLAST score 491
 E value 2.0e-49
 Match length 95
 % identity 92
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 399982
 Seq. ID LIB3431-029-P1-K1-D3
 Method BLASTX
 NCBI GI g482311
 BLAST score 707
 E value 8.0e-75

Match length 142
 % identity 97
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 399983
 Seq. ID LIB3431-029-P1-K1-D8
 Method BLASTX
 NCBI GI g132105
 BLAST score 565
 E value 3.0e-58
 Match length 124
 % identity 85
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399984
 Seq. ID LIB3431-029-P1-K1-E10
 Method BLASTX
 NCBI GI g132105
 BLAST score 609
 E value 2.0e-63
 Match length 131
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399985
 Seq. ID LIB3431-029-P1-K1-E11
 Method BLASTX
 NCBI GI g1617206
 BLAST score 190
 E value 6.0e-23
 Match length 74
 % identity 76
 NCBI Description (Z72489) CP12 [Pisum sativum]

Seq. No. 399986
 Seq. ID LIB3431-029-P1-K1-E12
 Method BLASTX
 NCBI GI g2407281
 BLAST score 497

NCBI Description (AC006841) putative serine/threonine protein kinase
[Arabidopsis thaliana]

Seq. No. 399992
Seq. ID LIB3431-029-P1-K1-F12
Method BLASTX
NCBI GI g3063447
BLAST score 244
E value 2.0e-33
Match length 155
% identity 24
NCBI Description (AC003981) F22013.9 [Arabidopsis thaliana]

Seq. No. 399993
Seq. ID LIB3431-029-P1-K1-F2
Method BLASTX
NCBI GI g1617197
BLAST score 304
E value 1.0e-27
Match length 76
% identity 76
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399994
Seq. ID LIB3431-029-P1-K1-F3
Method BLASTN
NCBI GI g2407266
BLAST score 102
E value 3.0e-50
Match length 158
% identity 91
NCBI Description Oryza sativa low molecular early light-inducible protein
mRNA, complete cds

Seq. No. 399995
Seq. ID LIB3431-029-P1-K1-F4
Method BLASTX
NCBI GI g729478
BLAST score 230
E value 5.0e-19
Match length 120
% identity 42
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
>gi_442481_dbj_BAA04616 (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
(AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
a region of the predicted gene.; similar to
ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 399996
Seq. ID LIB3431-029-P1-K1-F5
Method BLASTX
NCBI GI g3789954
BLAST score 654
E value 1.0e-68
Match length 121
% identity 100

00634015.101000

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399997
Seq. ID LIB3431-029-P1-K1-F6
Method BLASTX
NCBI GI g2570511
BLAST score 514
E value 2.0e-52
Match length 98
% identity 99

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 399998
Seq. ID LIB3431-029-P1-K1-F8
Method BLASTX
NCBI GI g131176
BLAST score 322
E value 9.0e-30
Match length 62
% identity 98

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
>gi_72683_pir_F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No. 399999
Seq. ID LIB3431-029-P1-K1-F9
Method BLASTX
NCBI GI g3850621
BLAST score 450
E value 9.0e-45
Match length 127
% identity 69

NCBI Description (Y15382) putative RNA binding protein [Arabidopsis thaliana]

Seq. No. 400000
Seq. ID LIB3431-029-P1-K1-G10
Method BLASTX
NCBI GI g3075488
BLAST score 713
E value 1.0e-75
Match length 143
% identity 97

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 400001
Seq. ID LIB3431-029-P1-K1-G11
Method BLASTX
NCBI GI g4406764
BLAST score 293
E value 3.0e-26
Match length 80

Seq. No. 400012
 Seq. ID LIB3431-029-P1-K1-H3
 Method BLASTX
 NCBI GI g132105
 BLAST score 546
 E value 6.0e-56
 Match length 122
 % identity 84
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400013
 Seq. ID LIB3431-029-P1-K1-H5
 Method BLASTN
 NCBI GI g168500
 BLAST score 62
 E value 3.0e-26
 Match length 118
 % identity 88
 NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds

Seq. No. 400014
 Seq. ID LIB3431-029-P1-K1-H7
 Method BLASTX
 NCBI GI g5926740
 BLAST score 455
 E value 2.0e-45
 Match length 89
 % identity 98
 NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]

Seq. No. 400015
 Seq. ID LIB3431-029-P1-N1-A10
 Method BLASTX
 NCBI GI g2982362
 BLAST score 306
 E value 6.0e-28
 Match length 63
 % identity 89
 NCBI Description (AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No. 400016
 Seq. ID LIB3431-029-P1-N1-A2
 Method BLASTX
 NCBI GI g4469021
 BLAST score 271
 E value 6.0e-24
 Match length 75
 % identity 71

Method BLASTN
 NCBI GI g2662344
 BLAST score 319
 E value 1.0e-179
 Match length 323
 % identity 100
 NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 400023
 Seq. ID LIB3431-029-P1-N1-B2
 Method BLASTX
 NCBI GI g3183079
 BLAST score 180
 E value 2.0e-15
 Match length 62
 % identity 66
 NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
 >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
 dehydrogenase [Oryza sativa]

Seq. No. 400024
 Seq. ID LIB3431-029-P1-N1-B3
 Method BLASTN
 NCBI GI g600766
 BLAST score 329
 E value 0.0e+00
 Match length 368
 % identity 98
 NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

Seq. No. 400025
 Seq. ID LIB3431-029-P1-N1-B4
 Method BLASTN
 NCBI GI g218207
 BLAST score 135
 E value 6.0e-70
 Match length 199
 % identity 92
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS1139

Seq. No. 400026
 Seq. ID LIB3431-029-P1-N1-B6
 Method BLASTX
 NCBI GI g1076308
 BLAST score 156
 E value 2.0e-10
 Match length 74
 % identity 45
 NCBI Description RNA-binding protein cp33 precursor - Arabidopsis thaliana
 >gi_681910_dbj_BAA06522_ (D31714) cp33 [Arabidopsis
 thaliana] >gi_4886289_emb_CAB43448.1_ (AL050300)
 RNA-binding protein cp33 precursor [Arabidopsis thaliana]

Seq. No. 400027
 Seq. ID LIB3431-029-P1-N1-B9

Method BLASTN
 NCBI GI g20181
 BLAST score 66
 E value 1.0e-28
 Match length 126
 % identity 88
 NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 400028
 Seq. ID LIB3431-029-P1-N1-C3
 Method BLASTN
 NCBI GI g218171
 BLAST score 166
 E value 3.0e-88
 Match length 242
 % identity 93
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
 a/b binding protein of photosystem II (LHCPII), complete
 cds

Seq. No. 400029
 Seq. ID LIB3431-029-P1-N1-C4
 Method BLASTN
 NCBI GI g218154
 BLAST score 76
 E value 1.0e-34
 Match length 138
 % identity 99
 NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
 clone:Aldp

Seq. No. 400030
 Seq. ID LIB3431-029-P1-N1-C5
 Method BLASTN
 NCBI GI g218154
 BLAST score 84
 E value 2.0e-39
 Match length 124
 % identity 92
 NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
 clone:Aldp

Seq. No. 400031
 Seq. ID LIB3431-029-P1-N1-C8
 Method BLASTN
 NCBI GI g218209
 BLAST score 155
 E value 1.0e-81
 Match length 338
 % identity 96
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS2106

Seq. No. 400032
 Seq. ID LIB3431-029-P1-N1-D1

cds

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Seq. No.          400062
Seq. ID           LIB3431-029-P1-N1-H2
Method            BLASTX
NCBI GI           g687677
BLAST score       234
E value           1.0e-19
Match length      58
% identity        76
NCBI Description   (U19925) unknown [Arabidopsis thaliana]
```

```
Seq. No.      400063
Seq. ID      LIB3431-029-P1-N1-H3
Method       BLASTX
NCBI GI      g347451
BLAST score   173
E value      2.0e-12
Match length  33
% identity    100
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
sativa]
```

Seq. No.	400064
Seq. ID	LIB3431-029-P1-N1-H5
Method	BLASTX
NCBI GI	g223793
BLAST score	190
E value	2.0e-14
Match length	37
% identity	100
NCBI Description	histone H4 [Physarum polycephalum]

Seq. No.	400065
Seq. ID	LIB3431-029-P1-N1-H6
Method	BLASTN
NCBI GI	g20177
BLAST score	137
E value	3.0e-71
Match length	172
% identity	95
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	400066
Seq. ID	LIB3431-029-P1-N1-H7
Method	BLASTN
NCBI GI	g5926739
BLAST score	369
E value	0.0e+00
Match length	393
% identity	98
NCBI Description	Oryza sativa mRNA for asparaginyl endopeptidase, complete cds

Seq. No.	400067
Seq. ID	LIB3431-029-P1-N1-H9

Method	BLASTX
NCBI GI	g5103833
BLAST score	156
E value	1.0e-10
Match length	43
% identity	70
NCBI Description	(AC007591) ESTs gb_R65145, gb_N96612 and gb_R90096 come from this gene. [Arabidopsis thaliana]
Seq. No.	400068
Seq. ID	LIB3431-030-P1-K2-A11
Method	BLASTX
NCBI GI	g4586039
BLAST score	419
E value	4.0e-41
Match length	130
% identity	62
NCBI Description	(AC007109) unknown protein [Arabidopsis thaliana]
Seq. No.	400069
Seq. ID	LIB3431-030-P1-K2-A3
Method	BLASTN
NCBI GI	g4206059
BLAST score	33
E value	3.0e-09
Match length	33
% identity	100
NCBI Description	Homo sapiens map 20q13.3; 51cR from D20S173 repeat region, complete sequence
Seq. No.	400070
Seq. ID	LIB3431-030-P1-K2-A5
Method	BLASTN
NCBI GI	g5922603
BLAST score	84
E value	3.0e-39
Match length	107
% identity	95
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
Seq. No.	400071
Seq. ID	LIB3431-030-P1-K2-A6
Method	BLASTX
NCBI GI	g729479
BLAST score	473
E value	1.0e-47
Match length	105
% identity	84
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
Seq. No.	400072
Seq. ID	LIB3431-030-P1-K2-A7
Method	BLASTX
NCBI GI	g871931
BLAST score	204
E value	3.0e-16

Seq. No. 400078
 Seq. ID LIB3431-030-P1-K2-B8
 Method BLASTX
 NCBI GI g132105
 BLAST score 547
 E value 4.0e-56
 Match length 120
 % identity 86
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400079
 Seq. ID LIB3431-030-P1-K2-C10
 Method BLASTX
 NCBI GI g4678303
 BLAST score 184
 E value 1.0e-13
 Match length 52
 % identity 63
 NCBI Description (AL049655) putative protein [Arabidopsis thaliana]

Seq. No. 400080
 Seq. ID LIB3431-030-P1-K2-C11
 Method BLASTN
 NCBI GI g19086
 BLAST score 78
 E value 1.0e-35
 Match length 126
 % identity 91
 NCBI Description Hordeum vulgare pot. psaE mRNA

Seq. No. 400081
 Seq. ID LIB3431-030-P1-K2-C2
 Method BLASTN
 NCBI GI g19094
 BLAST score 54
 E value 1.0e-21
 Match length 66
 % identity 95
 NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No. 400082
 Seq. ID LIB3431-030-P1-K2-C4
 Method BLASTX
 NCBI GI g4678303
 BLAST score 205
 E value 4.0e-16
 Match length 57
 % identity 65
 NCBI Description (AL049655) putative protein [Arabidopsis thaliana]

Seq. ID LIB3431-030-P1-K2-D11
 Method BLASTX
 NCBI GI g1488297
 BLAST score 516
 E value 2.0e-52
 Match length 129
 % identity 84
 NCBI Description (U63530) osRAD23 [Oryza sativa]

Seq. No. 400089
 Seq. ID LIB3431-030-P1-K2-D2
 Method BLASTX
 NCBI GI g3121731
 BLAST score 642
 E value 3.0e-67
 Match length 143
 % identity 83
 NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_2145473_emb_CAA65735_ (X97012) aconitate hydratase [Solanum tuberosum]

Seq. No. 400090
 Seq. ID LIB3431-030-P1-K2-D3
 Method BLASTX
 NCBI GI g132105
 BLAST score 149
 E value 4.0e-10
 Match length 31
 % identity 97
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400091
 Seq. ID LIB3431-030-P1-K2-D4
 Method BLASTX
 NCBI GI g671740
 BLAST score 554
 E value 6.0e-57
 Match length 109
 % identity 95
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 400092
 Seq. ID LIB3431-030-P1-K2-D6
 Method BLASTX
 NCBI GI g1654144
 BLAST score 292
 E value 4.0e-37
 Match length 103

```
% identity      74
NCBI Description (U38471) small GTP-binding protein rab [Brassica rapa]
```

Seq. No.	400093
Seq. ID	LIB3431-030-P1-K2-D7
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	7.0e-11
Match length	35
% identity	100
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

```
Seq. No.      400094
Seq. ID      LIB3431-030-P1-K2-E10
Method       BLASTX
NCBI GI      g3023816
BLAST score   584
E value      2.0e-60
Match length 132
% identity    86
NCBI Description  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_968996 (U31676) glyceraldehyde-3-phosphate
dehydrogenase [Oryza sativa]
```

```
Seq. No.      400095
Seq. ID      LIB3431-030-P1-K2-E12
Method       BLASTX
NCBI GI      g1709620
BLAST score   505
E value      3.0e-51
Match length  116
% identity    82
NCBI Description  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_508975
                  (U11496) protein disulfide isomerase [Triticum aestivum]
                  >gi_1094851_prf_2106410A protein disulfide isomerase
                  [Triticum aestivum]
```

Seq. No.	400096
Seq. ID	LIB3431-030-P1-K2-E2
Method	BLASTN
NCBI GI	g167086
BLAST score	69
E value	1.0e-30
Match length	167
% identity	85
NCBI Description	Hordeum vulgare photosystem I protein (PSI-L) mRNA, complete cds

```
Seq. No.          400097
Seq. ID           LIB3431-030-P1-K2-E4
Method            BLASTX
NCBI GI           g132105
BLAST score       628
E value           7.0e-72
Match length      135
% identity        99
```


>gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
dehydrogenase [Oryza sativa]

Seq. No. 400102
Seq. ID LIB3431-030-P1-K2-F1
Method BLASTX
NCBI GI g133999
BLAST score 489
E value 2.0e-49
Match length 99
% identity 100
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir_R3RZ7
ribosomal protein S7 - rice chloroplast
>gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7
[Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal
protein S7 [Oryza sativa] >gi_226657_prf_1603356CH
ribosomal protein S7 [Oryza sativa]

Seq. No. 400103
Seq. ID LIB3431-030-P1-K2-F10
Method BLASTX
NCBI GI g132105
BLAST score 706
E value 1.0e-74
Match length 131
% identity 98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 400104
Seq. ID LIB3431-030-P1-K2-F12
Method BLASTX
NCBI GI g1519251
BLAST score 443
E value 6.0e-44
Match length 111
% identity 83
NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 400105
Seq. ID LIB3431-030-P1-K2-F2
Method BLASTN
NCBI GI g3789951
BLAST score 71
E value 3.0e-32
Match length 91
% identity 95
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
(Cab27) mRNA, nuclear gene encoding chloroplast protein,
complete cds

09584016.101000

Seq. No. 400106
 Seq. ID LIB3431-030-P1-K2-F4
 Method BLASTX
 NCBI GI g2570523
 BLAST score 567
 E value 2.0e-58
 Match length 128
 % identity 80
 NCBI Description (AF022873) inorganic phosphate transporter [Lycopersicon
 esculentum]

Seq. No. 400107
 Seq. ID LIB3431-030-P1-K2-F5
 Method BLASTX
 NCBI GI g134944
 BLAST score 718
 E value 6.0e-82
 Match length 179
 % identity 84
 NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
 (STEAROYL-ACP DESATURASE) >gi_100502_pir_A39173
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6)
 precursor - safflower >gi_167197 (M61109)
 stearyl-acyl-carrier protein desaturase [Carthamus
 tinctorius]

Seq. No. 400108
 Seq. ID LIB3431-030-P1-K2-F6
 Method BLASTX
 NCBI GI g3777598
 BLAST score 314
 E value 6.0e-29
 Match length 104
 % identity 67
 NCBI Description (AF095707) 30S ribosomal protein S17 [Oryza sativa]

Seq. No. 400109
 Seq. ID LIB3431-030-P1-K2-F7
 Method BLASTX
 NCBI GI g3789952
 BLAST score 279
 E value 1.0e-45
 Match length 102
 % identity 96
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
 sativa]

Seq. No. 400110
 Seq. ID LIB3431-030-P1-K2-F8
 Method BLASTX
 NCBI GI g3024697
 BLAST score 274
 E value 2.0e-24
 Match length 91
 % identity 65
 NCBI Description T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)

(CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No. 400111
Seq. ID LIB3431-030-P1-K2-F9
Method BLASTN
NCBI GI g20177
BLAST score 40
E value 2.0e-13
Match length 94
% identity 88
NCBI Description Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No. 400112
Seq. ID LIB3431-030-P1-K2-G1
Method BLASTX
NCBI GI g1084455
BLAST score 517
E value 1.0e-52
Match length 116
% identity 85
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 400113
Seq. ID LIB3431-030-P1-K2-G11
Method BLASTX
NCBI GI g4185499
BLAST score 167
E value 1.0e-11
Match length 65
% identity 49
NCBI Description (AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No. 400114
Seq. ID LIB3431-030-P1-K2-G5
Method BLASTX
NCBI GI g1353352
BLAST score 527
E value 1.0e-53
Match length 150
% identity 70
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 400115
Seq. ID LIB3431-030-P1-K2-G6
Method BLASTX
NCBI GI g2316016
BLAST score 198
E value 1.0e-18
Match length 86
% identity 60

protein [Oryza sativa]

Seq. No. 400135
 Seq. ID LIB3431-030-P1-N1-B4
 Method BLASTN
 NCBI GI g5734616
 BLAST score 409
 E value 0.0e+00
 Match length 499
 % identity 100
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No. 400136
 Seq. ID LIB3431-030-P1-N1-B5
 Method BLASTX
 NCBI GI g3345477
 BLAST score 331
 E value 9.0e-31
 Match length 62
 % identity 100
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 400137
 Seq. ID LIB3431-030-P1-N1-B7
 Method BLASTX
 NCBI GI g3510256
 BLAST score 229
 E value 9.0e-19
 Match length 79
 % identity 56
 NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 400138
 Seq. ID LIB3431-030-P1-N1-B8
 Method BLASTX
 NCBI GI g132105
 BLAST score 207
 E value 8.0e-23
 Match length 56
 % identity 93
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400139
 Seq. ID LIB3431-030-P1-N1-B9
 Method BLASTX
 NCBI GI g4115536
 BLAST score 293
 E value 2.0e-26
 Match length 114

Match length 60
 % identity 83
 NCBI Description (U63530) osRAD23 [Oryza sativa]

Seq. No. 400150
 Seq. ID LIB3431-030-P1-N1-D12
 Method BLASTX
 NCBI GI g461595
 BLAST score 183
 E value 2.0e-13
 Match length 95
 % identity 44
 NCBI Description ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
 >gi_479533_pir_S34473 H+-transporting ATP synthase (EC
 3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520
 (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]

Seq. No. 400151
 Seq. ID LIB3431-030-P1-N1-D2
 Method BLASTX
 NCBI GI g6093830
 BLAST score 164
 E value 2.0e-11
 Match length 50
 % identity 38
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
 [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
 PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
 putative photosystem II peptide [Spinacia oleracea]

Seq. No. 400152
 Seq. ID LIB3431-030-P1-N1-D3
 Method BLASTX
 NCBI GI g132105
 BLAST score 398
 E value 1.0e-38
 Match length 73
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400153
 Seq. ID LIB3431-030-P1-N1-D4
 Method BLASTX
 NCBI GI g132105
 BLAST score 301
 E value 2.0e-27
 Match length 57
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

Seq. ID	LIB3431-030-P1-N1-E12
Method	BLASTX
NCBI GI	g1709620
BLAST score	178
E value	9.0e-13
Match length	55
% identity	71
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_508975 (U11496) protein disulfide isomerase [Triticum aestivum] >gi_1094851_prf_2106410A protein disulfide isomerase [Triticum aestivum]
Seq. No.	400159
Seq. ID	LIB3431-030-P1-N1-E2
Method	BLASTX
NCBI GI	g131225
BLAST score	337
E value	2.0e-31
Match length	94
% identity	70
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]
Seq. No.	400160
Seq. ID	LIB3431-030-P1-N1-E4
Method	BLASTX
NCBI GI	g347451
BLAST score	152
E value	7.0e-10
Match length	38
% identity	79
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]
Seq. No.	400161
Seq. ID	LIB3431-030-P1-N1-E6
Method	BLASTX
NCBI GI	g671740
BLAST score	512
E value	6.0e-52
Match length	94
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	400162
Seq. ID	LIB3431-030-P1-N1-E8
Method	BLASTX
NCBI GI	g5802606
BLAST score	498
E value	3.0e-50
Match length	104
% identity	86
NCBI Description	(AF174486) methylenetetrahydrofolate reductase [Zea mays]

```
Seq. No.      400163
Seq. ID      LIB3431-030-P1-N1-E9
Method       BLASTX
NCBI GI      g3183079
BLAST score   341
E value      6.0e-32
Match length  83
% identity   78
NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
                >gi_1375075_dbj_BAA12870.1_(D85763) glyoxysomal malate
                dehydrogenase [Oryza sativa]
```

```
Seq. No.      400164
Seq. ID      LIB3431-030-P1-N1-F1
Method       BLASTX
NCBI GI      g1173275
BLAST score   590
E value      4.0e-61
Match length  136
% identity    90
NCBI Description  CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
                >gi_2119068_pir_S58630 ribosomal protein S7 - maize
                chloroplast>gi_902274_emb_CAA60339_ (X86563) ribosomal
                protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
                ribosomal protein S7 [Zea mays]
```

```
Seq. No.      2400165
Seq. ID      LIB3431-030-P1-N1-F10
Method       BLASTX
NCBI GI      g132105
BLAST score   386
E value      1.0e-47
Match length  93
% identity    100
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose biphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.      400166
Seq. ID      LIB3431-030-P1-N1-F12
Method       BLASTX
NCBI GI      g1519251
BLAST score   244
E value      1.0e-20
Match length  47
% identity    100
NCBI Description (U65957) GF14-c protein [Oryza sativa]
```

Seq. No.	400167
Seq. ID	LIB3431-030-P1-N1-F2
Method	BLASTX

NCBI GI g1587206
 BLAST score 186
 E value 1.0e-13
 Match length 39
 % identity 97
 NCBI Description T complex protein [Cucumis sativus]

Seq. No. 400168
 Seq. ID LIB3431-030-P1-N1-F4
 Method BLASTX
 NCBI GI g5053118
 BLAST score 495
 E value 5.0e-58
 Match length 165
 % identity 72
 NCBI Description (AF156695) inorganic phosphate transporter [Solanum tuberosum]

Seq. No. 400169
 Seq. ID LIB3431-030-P1-N1-F5
 Method BLASTX
 NCBI GI g2281099
 BLAST score 181
 E value 3.0e-13
 Match length 45
 % identity 76
 NCBI Description (AC002333) stearyl-ACP desaturase [Arabidopsis thaliana]

Seq. No. 400170
 Seq. ID LIB3431-030-P1-N1-F6
 Method BLASTX
 NCBI GI g3777598
 BLAST score 327
 E value 2.0e-30
 Match length 78
 % identity 85
 NCBI Description (AF095707) 30S ribosomal protein S17 [Oryza sativa]

Seq. No. 400171
 Seq. ID LIB3431-030-P1-N1-F7
 Method BLASTX
 NCBI GI g3789952
 BLAST score 230
 E value 6.0e-19
 Match length 44
 % identity 98
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 400172
 Seq. ID LIB3431-030-P1-N1-F9
 Method BLASTX
 NCBI GI g115787
 BLAST score 505
 E value 4.0e-51
 Match length 96
 % identity 100

E value 4.0e-49
 Match length 90
 % identity 99
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 400178
 Seq. ID LIB3431-030-P1-N1-H1
 Method BLASTN
 NCBI GI g1398998
 BLAST score 162
 E value 8.0e-86
 Match length 275
 % identity 97
 NCBI Description Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II, complete cds

Seq. No. 400179
 Seq. ID LIB3431-030-P1-N1-H10
 Method BLASTN
 NCBI GI g2331130
 BLAST score 259
 E value 1.0e-144
 Match length 271
 % identity 99
 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No. 400180
 Seq. ID LIB3431-030-P1-N1-H2
 Method BLASTX
 NCBI GI g3036951
 BLAST score 451
 E value 9.0e-45
 Match length 86
 % identity 99
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 400181
 Seq. ID LIB3431-030-P1-N1-H3
 Method BLASTX
 NCBI GI g417260
 BLAST score 303
 E value 2.0e-27
 Match length 77
 % identity 74
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 400182
 Seq. ID LIB3431-030-P1-N1-H6
 Method BLASTX
 NCBI GI g4079798
 BLAST score 301
 E value 2.0e-27

Match length 61
 % identity 93
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 400183
 Seq. ID LIB3431-030-P1-N1-H8
 Method BLASTN
 NCBI GI g3377792
 BLAST score 269
 E value 1.0e-149
 Match length 399
 % identity 92
 NCBI Description Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 400184
 Seq. ID LIB3431-030-P1-N1-H9
 Method BLASTX
 NCBI GI g6093827
 BLAST score 156
 E value 2.0e-10
 Match length 61
 % identity 29
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_2956690_emb_CAA11248_ (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) Psby precursor [Arabidopsis thaliana]

Seq. No. 400185
 Seq. ID LIB3431-031-P1-K1-A11
 Method BLASTX
 NCBI GI g2913893
 BLAST score 262
 E value 8.0e-23
 Match length 56
 % identity 82
 NCBI Description (AB011368) LIP5 [Oryza sativa]

Seq. No. 400186
 Seq. ID LIB3431-031-P1-K1-A12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 8.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 400187
 Seq. ID LIB3431-031-P1-K1-A2
 Method BLASTX
 NCBI GI g134595
 BLAST score 236

E value 1.0e-19
 Match length 71
 % identity 66
 NCBI Description SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir_S22508
 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice
 >gi_218224_dbj_BAA00799 (D00999) copper/zinc-superoxide
 dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic
 copper/zinc-superoxide dismutase [Oryza sativa]
 >gi_1096504_prf_2111424A Cu/Zn superoxide dismutase [Oryza
 sativa]

Seq. No. 400188
 Seq. ID LIB3431-031-P1-K1-A3
 Method BLASTN
 NCBI GI g19094
 BLAST score 53
 E value 9.0e-21
 Match length 65
 % identity 95
 NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No. 400189
 Seq. ID LIB3431-031-P1-K1-A4
 Method BLASTN
 NCBI GI g20262
 BLAST score 193
 E value 1.0e-104
 Match length 300
 % identity 100
 NCBI Description O.sativa light-induced mRNA

Seq. No. 400190
 Seq. ID LIB3431-031-P1-K1-A5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 641
 E value 3.0e-67
 Match length 120
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 400191
 Seq. ID LIB3431-031-P1-K1-A6
 Method BLASTX
 NCBI GI g4914452
 BLAST score 420
 E value 3.0e-41
 Match length 127
 % identity 62
 NCBI Description (AL050398) putative protein [Arabidopsis thaliana]

Seq. No. 400192
 Seq. ID LIB3431-031-P1-K1-A7
 Method BLASTX
 NCBI GI g134595
 BLAST score 615

```
E value          4.0e-64
Match length     116
% identity       100
NCBI Description SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir_S22508
                 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice
                 >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide
                 dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic
                 copper/zinc-superoxide dismutase [Oryza sativa]
                 >gi_1096504_prf_2111424A Cu/Zn superoxide dismutase [Oryza
                 sativa]
```

```
Seq. No.          400193
Seq. ID           LIB3431-031-P1-K1-A8
Method            BLASTX
NCBI GI           g5903036
BLAST score       316
E value           4.0e-29
Match length      132
% identity        52
NCBI Description   (AC008016) F6D8.5 [Arabidopsis thaliana]
```

Seq. No.	400194
Seq. ID	LIB3431-031-P1-K1-B1
Method	BLASTX
NCBI GI	g5702231
BLAST score	195
E value	7.0e-15
Match length	110
% identity	45
NCBI Description	(AF145386) hypersensitive reaction associated Ca2+-binding protein [Phaseolus vulgaris]

```
Seq. No.          400195
Seq. ID           LIB3431-031-P1-K1-B10
Method            BLASTX
NCBI GI           g320618
BLAST score       285
E value           5.0e-26
Match length      62
% identity        89
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
```

Seq. No.	400196
Seq. ID	LIB3431-031-P1-K1-B2
Method	BLASTX
NCBI GI	g2754849
BLAST score	254
E value	7.0e-22
Match length	56
% identity	88
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

000001-101000

Seq. No. 400197
Seq. ID LIB3431-031-P1-K1-B9
Method BLASTN
NCBI GI g4138289
BLAST score 177
E value 8.0e-95
Match length 281
% identity 91
NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 400198
Seq. ID LIB3431-031-P1-K1-C1
Method BLASTX
NCBI GI g228403
BLAST score 655
E value 8.0e-69
Match length 145
% identity 89
NCBI Description glycolate oxidase [Lens culinaris]

Seq. No. 400199
Seq. ID LIB3431-031-P1-K1-C12
Method BLASTX
NCBI GI g132105
BLAST score 577
E value 1.0e-59
Match length 124
% identity 87
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR.
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 400200
Seq. ID LIB3431-031-P1-K1-C2
Method BLASTX
NCBI GI g320618
BLAST score 536
E value 7.0e-55
Match length 118
% identity 86
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 400201
Seq. ID LIB3431-031-P1-K1-C3
Method BLASTX
NCBI GI g2072555
BLAST score 237

Seq. No. 400220
 Seq. ID LIB3431-031-P1-K1-F9
 Method BLASTX
 NCBI GI g82080
 BLAST score 333
 E value 4.0e-31
 Match length 104
 % identity 64
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 400221
 Seq. ID LIB3431-031-P1-K1-G3
 Method BLASTX
 NCBI GI g132105
 BLAST score 600
 E value 2.0e-62
 Match length 129
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400222
 Seq. ID LIB3431-031-P1-K1-G4
 Method BLASTX
 NCBI GI g2130127
 BLAST score 397
 E value 1.0e-38
 Match length 92
 % identity 84
 NCBI Description ferritin 1 precursor - maize >gi_1103628_emb_CAA58146_
 (X83076) ferritin [Zea mays]

Seq. No. 400223
 Seq. ID LIB3431-031-P1-K1-G5
 Method BLASTX
 NCBI GI g115787
 BLAST score 614
 E value 5.0e-64
 Match length 137
 % identity 89
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109_
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 400224
 Seq. ID LIB3431-031-P1-K1-H11

Method	BLASTX
NCBI GI	g217909
BLAST score	353
E value	2.0e-33
Match length	105
% identity	69
NCBI Description	(D14044) glycolate oxidase [Cucurbita sp.]
Seq. No.	400225
Seq. ID	LIB3431-031-P1-N1-A3
Method	BLASTX
NCBI GI	g3914466
BLAST score	472
E value	2.0e-47
Match length	90
% identity	96
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_2981214 (AF052429) photosystem I complex Psan subunit precursor [Zea mays]
Seq. No.	400226
Seq. ID	LIB3431-031-P1-N1-A4
Method	BLASTX
NCBI GI	g417260
BLAST score	338
E value	2.0e-31
Match length	115
% identity	62
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]
Seq. No.	400227
Seq. ID	LIB3431-031-P1-N1-A5
Method	BLASTX
NCBI GI	g671740
BLAST score	227
E value	2.0e-18
Match length	45
% identity	96
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	400228
Seq. ID	LIB3431-031-P1-N1-A6
Method	BLASTX
NCBI GI	g4914452
BLAST score	274
E value	6.0e-24
Match length	75
% identity	68
NCBI Description	(AL050398) putative protein [Arabidopsis thaliana]
Seq. No.	400229
Seq. ID	LIB3431-031-P1-N1-A7
Method	BLASTX
NCBI GI	g538430

```
BLAST score      279
E value         1.0e-24
Match length    55
% identity      98
NCBI Description (L36320) superoxide dismutase [Oryza sativa]
```

```
Seq. No.      400230
Seq. ID      LIB3431-031-P1-N1-B10
Method       BLASTX
NCBI GI      g115787
BLAST score   632
E value      6.0e-66
Match length  121
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.          400231
Seq. ID           LIB3431-031-P1-N1-B11
Method            BLASTN
NCBI GI           g218171
BLAST score       80
E value           3.0e-37
Match length      168
% identity        88
NCBI Description   Oryza sativa mRNA for type I light-harvesting chlorophyll
                  a/b binding protein of photosystem II (LHCPII), complete
                  cds
```

```
Seq. No.      400232
Seq. ID       LIB3431-031-P1-N1-B5
Method        BLASTN
NCBI GI       g2062705
BLAST score   33
E value       3.0e-09
Match length  41
% identity    95
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
```

```
Seq. No.      400233
Seq. ID      LIB3431-031-P1-N1-B8
Method       BLASTX
NCBI GI      g5734790
BLAST score   335
E value      2.0e-31
Match length  76
% identity    86
NCBI Description (AC007980) ATP-dependent metalloprotease [Arabidopsis
thaliana]
```

Seq. No.	400234
Seq. ID	LIB3431-031-P1-N1-B9
Method	BLASTX
NCBI GI	q4138290

BLAST score 398
 E value 1.0e-38
 Match length 77
 % identity 100
 NCBI Description (AJ005841) thioredoxin M [Oryza sativa]

Seq. No. 400235
 Seq. ID LIB3431-031-P1-N1-C1
 Method BLASTX
 NCBI GI g2570515
 BLAST score 196
 E value 5.0e-15
 Match length 41
 % identity 93
 NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 400236
 Seq. ID LIB3431-031-P1-N1-C10
 Method BLASTX
 NCBI GI g131397
 BLAST score 158
 E value 2.0e-10
 Match length 147
 % identity 28
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
 >gi_81480_pir_S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach
 >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi_225597_prf_1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No. 400237
 Seq. ID LIB3431-031-P1-N1-C12
 Method BLASTN
 NCBI GI g218207
 BLAST score 327
 E value 0.0e+00
 Match length 399
 % identity 95
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 400238
 Seq. ID LIB3431-031-P1-N1-C2
 Method BLASTX
 NCBI GI g115787
 BLAST score 432
 E value 1.0e-42
 Match length 82
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

09634016 103000

Seq. No.	400243
Seq. ID	LIB3431-031-P1-N1-D1
Method	BLASTN

NCBI GI	g3885887
BLAST score	425
E value	0.0e+00
Match length	429
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

```
Seq. No.      400249
Seq. ID       LIB3431-031-P1-N1-E12
Method        BLASTX
NCBI GI       g1076422
BLAST score    229
E value       1.0e-18
Match length   85
% identity     60
NCBI Description transcription factor OBF4 - Arabidopsis thaliana
               >gi_414613_emb_CAA49524_(X69899) ocs-element binding
               factor 4 [Arabidopsis thaliana]
```

```
Seq. No.      400250
Seq. ID      LIB3431-031-P1-N1-E2
Method       BLASTX
NCBI GI      g133019
BLAST score   256
E value      4.0e-22
Match length  79
% identity    56
NCBI Description 60S RIBOSOMAL PROTEIN L7 >gi_71122_pir_R5D07 ribosomal
protein L7 - slime mold (Dictyostelium discoideum)
>gi_7357_emb_CAA33035_(X14909) ribosomal protein L7 (AA 1
- 246) [Dictyostelium discoideum]
```

Seq. No.	400251
Seq. ID	LIB3431-031-P1-N1-E4
Method	BLASTX
NCBI GI	g3126854
BLAST score	507
E value	1.0e-68
Match length	135
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

```
Seq. No.      400252
Seq. ID      LIB3431-031-P1-N1-E6
Method       BLASTN
NCBI GI      g218209
BLAST score   53
E value      9.0e-21
Match length  69
% identity    94
NCBI Description  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
```

Seq. No. 400253
Seq. ID LIB3431-031-P1-N1-E8

>gi_478404_pir_JQ2247 photosystem I chain D precursor -
barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 400267
Seq. ID LIB3431-031-P1-N1-H1
Method BLASTX
NCBI GI g4886443
BLAST score 219
E value 1.0e-17
Match length 62
% identity 76
NCBI Description (AL050268) hypothetical protein [Homo sapiens]

Seq. No. 400268
Seq. ID LIB3431-031-P1-N1-H11
Method BLASTX
NCBI GI g1486472
BLAST score 168
E value 9.0e-12
Match length 33
% identity 85
NCBI Description (X99853) oxoglutarate malate translocator [Solanum
tuberosum]

Seq. No. 400269
Seq. ID LIB3431-031-P1-N1-H12
Method BLASTX
NCBI GI g2570515
BLAST score 148
E value 2.0e-09
Match length 38
% identity 71
NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 400270
Seq. ID LIB3431-031-P1-N1-H6
Method BLASTX
NCBI GI g733454
BLAST score 446
E value 3.0e-44
Match length 91
% identity 95
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 400271
Seq. ID LIB3431-031-P1-N1-H7
Method BLASTN
NCBI GI g5295987
BLAST score 124
E value 4.0e-63
Match length 359
% identity 84
NCBI Description Oryza sativa mRNA for MADS box-like protein, complete cds,
clone:S10304

Seq. No. 400272

NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 400277
Seq. ID LIB3431-033-P1-K1-A4
Method BLASTX
NCBI GI g2286153
BLAST score 529
E value 4.0e-60
Match length 138
% identity 80
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 400278
Seq. ID LIB3431-033-P1-K1-A6
Method BLASTX
NCBI GI g1419090
BLAST score 431
E value 1.0e-42
Match length 116
% identity 72
NCBI Description (X94968) 37kDa chloroplast inner envelope membrane
polypeptide precursor [Nicotiana tabacum]

Seq. No. 400279
Seq. ID LIB3431-033-P1-K1-A7
Method BLASTX
NCBI GI g710308
BLAST score 377
E value 3.0e-36
Match length 72
% identity 94
NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 400280
Seq. ID LIB3431-033-P1-K1-A8
Method BLASTX
NCBI GI g5733866
BLAST score 442
E value 8.0e-44
Match length 140
% identity 62
NCBI Description (AC007932) Contains similarity to gb_M73488
1-aminocyclopropane-1-carboxylate deaminase from
Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from
this gene. [Arabidopsis thaliana]

Seq. No. 400281
Seq. ID LIB3431-033-P1-K1-A9
Method BLASTN
NCBI GI g218207
BLAST score 246
E value 1.0e-136
Match length 246
% identity 100
NCBI Description Oryza sativa mRNA for the small subunit of

096016

Seq. No.	400296
Seq. ID	LIB3431-033-P1-K1-D11
Method	BLASTX

NCBI GI g3885888
 BLAST score 180
 E value 4.0e-13
 Match length 83
 % identity 52
 NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 400297
 Seq. ID LIB3431-033-P1-K1-D12
 Method BLASTX
 NCBI GI g2407281
 BLAST score 674
 E value 5.0e-71
 Match length 127
 % identity 98
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 400298
 Seq. ID LIB3431-033-P1-K1-D2
 Method BLASTN
 NCBI GI g20262
 BLAST score 225
 E value 1.0e-123
 Match length 225
 % identity 100
 NCBI Description O.sativa light-induced mRNA

Seq. No. 400299
 Seq. ID LIB3431-033-P1-K1-D4
 Method BLASTX
 NCBI GI g5729802
 BLAST score 254
 E value 8.0e-22
 Match length 53
 % identity 83
 NCBI Description similar to S. pombe diml+ >gi_2565275 (AF023611) Dimlp homolog [Homo sapiens]

Seq. No. 400300
 Seq. ID LIB3431-033-P1-K1-D5
 Method BLASTX
 NCBI GI g1169798
 BLAST score 688
 E value 1.0e-72
 Match length 145
 % identity 92
 NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B) (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218) phosphoglucose isomerase (Pgi-b) [Oryza sativa]

Seq. No. 400301
 Seq. ID LIB3431-033-P1-K1-D6
 Method BLASTX
 NCBI GI g3345477
 BLAST score 662

E value 1.0e-69
 Match length 125
 % identity 100
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 400302
 Seq. ID LIB3431-033-P1-K1-D7
 Method BLASTX
 NCBI GI g5923670
 BLAST score 296
 E value 8.0e-27
 Match length 99
 % identity 57
 NCBI Description (AC009326) unknown protein [Arabidopsis thaliana]

Seq. No. 400303
 Seq. ID LIB3431-033-P1-K1-D8
 Method BLASTX
 NCBI GI g3885513
 BLAST score 276
 E value 2.0e-24
 Match length 74
 % identity 62
 NCBI Description (AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No. 400304
 Seq. ID LIB3431-033-P1-K1-E1
 Method BLASTX
 NCBI GI g3980417
 BLAST score 385
 E value 4.0e-37
 Match length 118
 % identity 32
 NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 400305
 Seq. ID LIB3431-033-P1-K1-E10
 Method BLASTN
 NCBI GI g3885891
 BLAST score 121
 E value 2.0e-61
 Match length 170
 % identity 99
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 400306
 Seq. ID LIB3431-033-P1-K1-E11
 Method BLASTX
 NCBI GI g132105
 BLAST score 579
 E value 7.0e-60
 Match length 106
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400307
Seq. ID LIB3431-033-P1-K1-E12
Method BLASTX
NCBI GI g82080
BLAST score 436
E value 4.0e-43
Match length 124
% identity 68
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 400308
Seq. ID LIB3431-033-P1-K1-E3
Method BLASTX
NCBI GI g3345477
BLAST score 630
E value 6.0e-66
Match length 135
% identity 90
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 400309
Seq. ID LIB3431-033-P1-K1-E4
Method BLASTX
NCBI GI g417260
BLAST score 410
E value 5.0e-40
Match length 128
% identity 65
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No. 400310
Seq. ID LIB3431-033-P1-K1-E5
Method BLASTX
NCBI GI g115787
BLAST score 376
E value 4.0e-36
Match length 73
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 400311

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Seq. ID      LIB3431-033-P1-K1-E6
Method       BLASTX
NCBI GI      g115787
BLAST score   491
E value      1.0e-49
Match length  121
% identity    83
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
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```
Seq. No.      400312
Seq. ID      LIB3431-033-P1-K1-E7
Method       BLASTX
NCBI GI      g3126854
BLAST score   634
E value      2.0e-66
Match length  124
% identity    97
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
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Seq. No.      400313
Seq. ID      LIB3431-033-P1-K1-E8
Method       BLASTX
NCBI GI      g132105
BLAST score   426
E value      6.0e-42
Match length  77
% identity    100
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose biphosphate
                  carboxylase S [Oryza sativa]
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Seq. No.          400314
Seq. ID           LIB3431-033-P1-K1-E9
Method            BLASTX
NCBI GI           g2072555
BLAST score       237
E value           9.0e-20
Match length      44
% identity        100
NCBI Description   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
```

Seq. No.	400315
Seq. ID	LIB3431-033-P1-K1-F1
Method	BLASTX
NCBI GI	q3249064

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326
(M88321) Group 4 late embryogenesis-abundant protein
[Gossypium hirsutum] >gi_167328 (M88322) Group 4 late
embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 400336
Seq. ID LIB3431-033-P1-K1-H2
Method BLASTX
NCBI GI g2570511
BLAST score 580
E value 4.0e-60
Match length 111
% identity 98
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 400337
Seq. ID LIB3431-033-P1-K1-H4
Method BLASTN
NCBI GI g2072554
BLAST score 173
E value 1.0e-92
Match length 249
% identity 92
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
cds

Seq. No. 400338
Seq. ID LIB3431-033-P1-K1-H7
Method BLASTX
NCBI GI g132105
BLAST score 582
E value 3.0e-60
Match length 125
% identity 87
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 400339
Seq. ID LIB3431-033-P1-K1-H9
Method BLASTX
NCBI GI g170131
BLAST score 383
E value 6.0e-37
Match length 98
% identity 71
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 400340
Seq. ID LIB3431-033-P1-N1-A1
Method BLASTX

Match length 321
 % identity 99
 NCBI Description Rice cab1R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 400351
 Seq. ID LIB3431-033-P1-N1-B5
 Method BLASTX
 NCBI GI g1421730
 BLAST score 201
 E value 1.0e-15
 Match length 40
 % identity 95
 NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 400352
 Seq. ID LIB3431-033-P1-N1-C11
 Method BLASTX
 NCBI GI g3281853
 BLAST score 200
 E value 1.0e-15
 Match length 70
 % identity 59
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 400353
 Seq. ID LIB3431-033-P1-N1-C2
 Method BLASTN
 NCBI GI g6006355
 BLAST score 221
 E value 1.0e-121
 Match length 331
 % identity 100
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 400354
 Seq. ID LIB3431-033-P1-N1-C4
 Method BLASTX
 NCBI GI g551047
 BLAST score 209
 E value 1.0e-16
 Match length 42
 % identity 93
 NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 400355
 Seq. ID LIB3431-033-P1-N1-C5
 Method BLASTN
 NCBI GI g218171
 BLAST score 72
 E value 2.0e-32
 Match length 112
 % identity 91
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
 a/b binding protein of photosystem II (LHCPII), complete
 cds

009684015-101000

Seq. No. 400356
 Seq. ID LIB3431-033-P1-N1-C6
 Method BLASTN
 NCBI GI g5091597
 BLAST score 33
 E value 4.0e-09
 Match length 45
 % identity 93
 NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence.

Seq. No. 400357
 Seq. ID LIB3431-033-P1-N1-C7
 Method BLASTX
 NCBI GI g482311
 BLAST score 171
 E value 3.0e-12
 Match length 33
 % identity 100
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 400358
 Seq. ID LIB3431-033-P1-N1-C8
 Method BLASTX
 NCBI GI g482311
 BLAST score 315
 E value 5.0e-29
 Match length 63
 % identity 100
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 400359
 Seq. ID LIB3431-033-P1-N1-D1
 Method BLASTN
 NCBI GI g3789953
 BLAST score 317
 E value 1.0e-178
 Match length 317
 % identity 100
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 400360
 Seq. ID LIB3431-033-P1-N1-D11
 Method BLASTN
 NCBI GI g3885887
 BLAST score 297
 E value 1.0e-166
 Match length 301
 % identity 100
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds


```

NCBI GI      g4689380
BLAST score   258
E value       3.0e-22
Match length  52
% identity    94
NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein
[Vigna radiata]

```

```
Seq. No.      400391
Seq. ID      LIB3431-033-P1-N1-H4
Method       BLASTN
NCBI GI      g2072554
BLAST score   290
E value      1.0e-162
Match length  294
% identity    100
NCBI Description  Oryza sativa metallothionein-like protein mRNA, complete cds
```

```

Seq. No.      400392
Seq. ID      LIB3431-033-P1-N1-H7
Method       BLASTX
NCBI GI      g132105
BLAST score   301
E value      2.0e-27
Match length  57
% identity   100
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

```

```
Seq. No.      400393
Seq. ID      LIB3431-033-P1-N1-H9
Method       BLASTX
NCBI GI      g170131
BLAST score   152
E value      6.0e-10
Match length  47
% identity    64
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
```

Seq. No.	400394
Seq. ID	LIB3431-034-P1-K1-A11
Method	BLASTX
NCBI GI	g4469021
BLAST score	268
E value	2.0e-23
Match length	78
% identity	69
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.          400395
Seq. ID           LIB3431-034-P1-K1-A12
Method            BLASTX
NCBI GI           g1835731
BLAST score       310
E value           2.0e-28
Match length      71
% identity        83
NCBI Description  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

```
Seq. No.      400396
Seq. ID      LIB3431-034-P1-K1-A2
Method       BLASTX
NCBI GI      g548605
BLAST score   522
E value      3.0e-53
Match length  114
% identity    91
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                >gi_539055_pir_A48527 photosystem I protein psaK precursor
                - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                [Hordeum vulgare]
```

```
Seq. No.      400397
Seq. ID      LIB3431-034-P1-K1-A3
Method       BLASTX
NCBI GI      g3080375
BLAST score   386
E value      3.0e-37
Match length  118
% identity    64
NCBI Description (AL022580) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          400398
Seq. ID           LIB3431-034-P1-K1-A4
Method            BLASTN
NCBI GI           g6015437
BLAST score       36
E value           1.0e-10
Match length      47
% identity        65
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
```

Seq. No.	400399
Seq. ID	LIB3431-034-P1-K1-A6
Method	BLASTX
NCBI GI	g3420055
BLAST score	294
E value	2.0e-26
Match length	62
% identity	89
NCBI Description	(AC004680) cyclophilin [Arabidopsis thaliana]

```
Seq. No.      400400
Seq. ID      LIB3431-034-P1-K1-A7
Method       BLASTN
```


000T0T-9T048960

% identity 56
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 400429
Seq. ID LIB3431-034-P1-K1-E7
Method BLASTX
NCBI GI g2104959
BLAST score 188
E value 4.0e-14
Match length 42
% identity 81
NCBI Description (U96925) immunophilin [Vicia faba]

Seq. No. 400430
Seq. ID LIB3431-034-P1-K1-E9
Method BLASTN
NCBI GI g218171
BLAST score 159
E value 4.0e-84
Match length 279
% identity 89
NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No. 400431
Seq. ID LIB3431-034-P1-K1-F1
Method BLASTX
NCBI GI g320618
BLAST score 435
E value 4.0e-43
Match length 89
% identity 94
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 400432
Seq. ID LIB3431-034-P1-K1-F11
Method BLASTX
NCBI GI g3913018
BLAST score 723
E value 8.0e-77
Match length 139
% identity 99
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 400433
Seq. ID LIB3431-034-P1-K1-F12
Method BLASTX
NCBI GI g283971
BLAST score 365
E value 8.0e-35

Match length 137
 % identity 51
 NCBI Description aldehyde dehydrogenase (NAD(P)+) (EC 1.2.1.5) 3 - human
 >gi_178375 (M77477) aldehyde dehydrogenase [Homo sapiens]
 >gi_300402_bbs_132241 (S61044) aldehyde dehydrogenase
 isozyme 3, ALDH3 {EC 1.2.1.3} [human, stomach, Peptide, 453
 aa] [Homo sapiens]

Seq. No. 400434
 Seq. ID LIB3431-034-P1-K1-F2
 Method BLASTX
 NCBI GI g6013233
 BLAST score 301
 E value 3.0e-27
 Match length 140
 % identity 41
 NCBI Description (AF183932) ionotropic glutamate receptor homolog
 [Arabidopsis thaliana]

Seq. No. 400435
 Seq. ID LIB3431-034-P1-K1-F4
 Method BLASTX
 NCBI GI g3126854
 BLAST score 675
 E value 4.0e-71
 Match length 127
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400436
 Seq. ID LIB3431-034-P1-K1-F5
 Method BLASTX
 NCBI GI g115794
 BLAST score 218
 E value 1.0e-17
 Match length 78
 % identity 60
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
 III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
 protein type III precursor (cab-13) - tomato
 >gi_19277_emb_CAA42818_ (X60275) LHCII type III
 [Lycopersicon esculentum]

Seq. No. 400437
 Seq. ID LIB3431-034-P1-K1-F6
 Method BLASTX
 NCBI GI g6006363
 BLAST score 271
 E value 7.0e-24
 Match length 51
 % identity 100
 NCBI Description (AP000559) ESTs AU078183(C62904),C73912(E21020) correspond
 to a region of the predicted gene.; Similar to water stress
 inducible protein (U74296) [Oryza sativa]

Seq. No. 400438
 Seq. ID LIB3431-034-P1-K1-F7

```
Method          BLASTX
NCBI GI         g82080
BLAST score     408
E value        7.0e-40
Match length    116
% identity      68
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf_1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```

```
Seq. No.          400439
Seq. ID          LIB3431-034-P1-K1-F8
Method           BLASTX
NCBI GI          g548605
BLAST score      550
E value          1.0e-56
Match length     124
% identity       88
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

```
Seq. No.          400440
Seq. ID           LIB3431-034-P1-K1-F9
Method            BLASTX
NCBI GI           g733454
BLAST score       247
E value           5.0e-21
Match length      67
% identity        76
NCBI Description  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
```

Seq. No.	400441
Seq. ID	LIB3431-034-P1-K1-G10
Method	BLASTX
NCBI GI	g2827533
BLAST score	158
E value	1.0e-10
Match length	70
% identity	50
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.      400442
Seq. ID       LIB3431-034-P1-K1-G11
Method        BLASTX
NCBI GI       g2407281
BLAST score   641
E value       3.0e-67
Match length  121
% identity    98
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]
```

Seq. No. 400443


```
Match length      66
% identity       47
NCBI Description  (AC002335) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.          400449
Seq. ID          LIB3431-034-P1-K1-H11
Method          BLASTX
NCBI GI         g548605
BLAST score      594
E value         1.0e-61
Match length     130
% identity       91
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

```
Seq. No.          400450
Seq. ID           LIB3431-034-P1-K1-H3
Method            BLASTX
NCBI GI           g417482
BLAST score       397
E value           1.0e-38
Match length      140
% identity        58
NCBI Description  PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX
                  FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS
                  PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir_JQ2254
                  farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta
                  chain - garden pea >gi_169049 (L08664) farnesyl-protein
                  transferase beta-subunit [Pisum sativum]
```

```
Seq. No.      400451
Seq. ID      LIB3431-034-P1-K1-H5
Method       BLASTX
NCBI GI      g6006429
BLAST score   298
E value      6.0e-27
Match length  118
% identity    49
NCBI Description (AJ242958) SPL1-Related3 protein [Arabidopsis thaliana]
```

```

Seq. No.          400452
Seq. ID           LIB3431-034-P1-K1-H7
Method            BLASTX
NCBI GI           g132105
BLAST score       547
E value           4.0e-56
Match length      119
% identity        87
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

```

000101 9101000

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400453
Seq. ID LIB3431-034-P1-K1-H9
Method BLASTN
NCBI GI g2073379
BLAST score 88
E value 5.0e-42
Match length 92
% identity 99
NCBI Description Rice CP26 mRNA, partial sequence

Seq. No. 400454
Seq. ID LIB3431-034-P1-N1-A11
Method BLASTX
NCBI GI g4469021
BLAST score 292
E value 4.0e-26
Match length 76
% identity 74
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 400455
Seq. ID LIB3431-034-P1-N1-A12
Method BLASTX
NCBI GI g1835731
BLAST score 273
E value 4.0e-24
Match length 65
% identity 82
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 400456
Seq. ID LIB3431-034-P1-N1-A2
Method BLASTN
NCBI GI g304219
BLAST score 49
E value 1.0e-18
Match length 71
% identity 92
NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 400457
Seq. ID LIB3431-034-P1-N1-A6
Method BLASTX
NCBI GI g3420055
BLAST score 260
E value 2.0e-22
Match length 55
% identity 89
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No. 400458
Seq. ID LIB3431-034-P1-N1-A8

BLAST score 231
E value 4.0e-19
Match length 57
% identity 70
NCBI Description CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169
(AF026473) calmodulin-related protein [Arabidopsis
thaliana]

Seq. No. 400469
Seq. ID LIB3431-034-P1-N1-C5
Method BLASTX
NCBI GI g1296955
BLAST score 300
E value 3.0e-27
Match length 54
% identity 46
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 400470
Seq. ID LIB3431-034-P1-N1-C7
Method BLASTN
NCBI GI g1661159
BLAST score 157
E value 5.0e-83
Match length 237
% identity 92
NCBI Description Oryza sativa chlorophyll a/b binding protein (kcd1895)
mRNA, complete cds

Seq. No. 400471
Seq. ID LIB3431-034-P1-N1-C8
Method BLASTN
NCBI GI g2072726
BLAST score 461
E value 0.0e+00
Match length 503
% identity 98
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 400472
Seq. ID LIB3431-034-P1-N1-C9
Method BLASTX
NCBI GI g3345477
BLAST score 211
E value 9.0e-17
Match length 44
% identity 91
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 400473
Seq. ID LIB3431-034-P1-N1-D10
Method BLASTN
NCBI GI g218218
BLAST score 85
E value 6.0e-40
Match length 112
% identity 95

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Seq. No.	400478
Seq. ID	LIB3431-034-P1-N1-D6
Method	BLASTX
NCBI GI	q992633

09634016.101000

Match length 279
% identity 98
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 400494
Seq. ID LIB3431-034-P1-N1-F6
Method BLASTN
NCBI GI g6006355
BLAST score 374
E value 0.0e+00
Match length 380
% identity 99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 400495
Seq. ID LIB3431-034-P1-N1-F7
Method BLASTX
NCBI GI g115813
BLAST score 215
E value 3.0e-17
Match length 48
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 400496
Seq. ID LIB3431-034-P1-N1-F8
Method BLASTN
NCBI GI g304219
BLAST score 40
E value 3.0e-13
Match length 68
% identity 90
NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 400497
Seq. ID LIB3431-034-P1-N1-F9
Method BLASTX
NCBI GI g733456
BLAST score 371
E value 2.0e-35
Match length 76
% identity 95
NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 400498
Seq. ID LIB3431-034-P1-N1-G11
Method BLASTN
NCBI GI g218209
BLAST score 149
E value 4.0e-78
Match length 328
% identity 97

% identity 75
 NCBI Description PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX
 FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS
 PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir_JQ2254
 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta
 chain - garden pea >gi_169049 (L08664) farnesyl-protein
 transferase beta-subunit [Pisum sativum]

Seq. No. 400504
 Seq. ID LIB3431-034-P1-N1-H4
 Method BLASTN
 NCBI GI g3819197
 BLAST score 47
 E value 4.0e-17
 Match length 103
 % identity 86
 NCBI Description Hordeum vulgare partial mRNA; clone cMWG0676.uni

Seq. No. 400505
 Seq. ID LIB3431-034-P1-N1-H7
 Method BLASTN
 NCBI GI g218207
 BLAST score 295
 E value 1.0e-165
 Match length 307
 % identity 99
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS1139

Seq. No. 400506
 Seq. ID LIB3431-035-P1-K1-A1
 Method BLASTX
 NCBI GI g548605
 BLAST score 471
 E value 3.0e-47
 Match length 98
 % identity 93
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 400507
 Seq. ID LIB3431-035-P1-K1-A12
 Method BLASTX
 NCBI GI g1171579
 BLAST score 239
 E value 5.0e-20
 Match length 91
 % identity 48
 NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 400508
 Seq. ID LIB3431-035-P1-K1-A2
 Method BLASTX

NCBI GI g2582822
 BLAST score 172
 E value 3.0e-12
 Match length 39
 % identity 82
 NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) .[Solanum tuberosum]

Seq. No. 400509
 Seq. ID LIB3431-035-P1-K1-A3
 Method BLASTX
 NCBI GI g728744
 BLAST score 271
 E value 2.0e-46
 Match length 132
 % identity 80
 NCBI Description AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390
 auxin-induced protein - common tobacco
 >gi_19799_emb_CAA39708_ (X56267) auxin-induced protein
 [Nicotiana tabacum]

Seq. No. 400510
 Seq. ID LIB3431-035-P1-K1-A7
 Method BLASTX
 NCBI GI g5912299
 BLAST score 464
 E value 8.0e-55
 Match length 123
 % identity 88
 NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

Seq. No. 400511
 Seq. ID LIB3431-035-P1-K1-B11
 Method BLASTX
 NCBI GI g1076724
 BLAST score 665
 E value 6.0e-70
 Match length 141
 % identity 85
 NCBI Description LHCI-680, photosystem I antenna protein - barley
 >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
 antenna protein [Hordeum vulgare]

Seq. No. 400512
 Seq. ID LIB3431-035-P1-K1-B3
 Method BLASTX
 NCBI GI g320618
 BLAST score 578
 E value 1.0e-59
 Match length 127
 % identity 87
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

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Seq. No. 400513
 Seq. ID LIB3431-035-P1-K1-B4
 Method BLASTX
 NCBI GI g3386621
 BLAST score 513
 E value 4.0e-52
 Match length 119
 % identity 83
 NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 400514
 Seq. ID LIB3431-035-P1-K1-B5
 Method BLASTX
 NCBI GI g3273202
 BLAST score 394
 E value 4.0e-38
 Match length 115
 % identity 74
 NCBI Description (AB010918) response reactor4 [Arabidopsis thaliana]

Seq. No. 400515
 Seq. ID LIB3431-035-P1-K1-B7
 Method BLASTN
 NCBI GI g20181
 BLAST score 92
 E value 6.0e-44
 Match length 243
 % identity 86
 NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No. 400516
 Seq. ID LIB3431-035-P1-K1-B8
 Method BLASTX
 NCBI GI g417488
 BLAST score 608
 E value 3.0e-63
 Match length 152
 % identity 75
 NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_100452_pir_A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum]

Seq. No. 400517
 Seq. ID LIB3431-035-P1-K1-B9
 Method BLASTX
 NCBI GI g115787
 BLAST score 600
 E value 3.0e-62
 Match length 135
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

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Seq. No. 400518
 Seq. ID LIB3431-035-P1-K1-C11
 Method BLASTX
 NCBI GI g2407281
 BLAST score 758
 E value 7.0e-81
 Match length 149
 % identity 95
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 400519
 Seq. ID LIB3431-035-P1-K1-C2
 Method BLASTX
 NCBI GI g100454
 BLAST score 664
 E value 7.0e-70
 Match length 146
 % identity 86
 NCBI Description photosystem II oxygen-evolving complex protein 1 - potato
 >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein
 of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 400520
 Seq. ID LIB3431-035-P1-K1-C3
 Method BLASTX
 NCBI GI g544437
 BLAST score 339
 E value 1.0e-31
 Match length 73
 % identity 86
 NCBI Description GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
 >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]

Seq. No. 400521
 Seq. ID LIB3431-035-P1-K1-C4
 Method BLASTN
 NCBI GI g473980
 BLAST score 76
 E value 9.0e-35
 Match length 113
 % identity 90
 NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene

Seq. No. 400522
 Seq. ID LIB3431-035-P1-K1-C6
 Method BLASTX
 NCBI GI g82080
 BLAST score 415
 E value 1.0e-40
 Match length 141
 % identity 62
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 400523
 Seq. ID LIB3431-035-P1-K1-C7
 Method BLASTX
 NCBI GI g3345477
 BLAST score 662
 E value 1.0e-69
 Match length 127
 % identity 98
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 400524
 Seq. ID LIB3431-035-P1-K1-C8
 Method BLASTX
 NCBI GI g5042462
 BLAST score 450
 E value 9.0e-45
 Match length 114
 % identity 80
 NCBI Description (AC007789) putative negatively light-regulated protein [Oryza sativa]

Seq. No. 400525
 Seq. ID LIB3431-035-P1-K1-C9
 Method BLASTX
 NCBI GI g132105
 BLAST score 676
 E value 3.0e-71
 Match length 144
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400526
 Seq. ID LIB3431-035-P1-K1-D1
 Method BLASTX
 NCBI GI g1173347
 BLAST score 793
 E value 6.0e-85
 Match length 153
 % identity 95
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 400527
 Seq. ID LIB3431-035-P1-K1-D10
 Method BLASTX

% identity 80
NCBI Description (U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No. 400557
Seq. ID LIB3431-035-P1-K1-G5
Method BLASTX
NCBI GI g5031281
BLAST score 314
E value 9.0e-29
Match length 98
% identity 62
NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 400558
Seq. ID LIB3431-035-P1-K1-G6
Method BLASTN
NCBI GI g1245938
BLAST score 35
E value 6.0e-10
Match length 35
% identity 100
NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No. 400559
Seq. ID LIB3431-035-P1-K1-G8
Method BLASTX
NCBI GI g3885888
BLAST score 347
E value 1.0e-32
Match length 70
% identity 97
NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 400560
Seq. ID LIB3431-035-P1-K1-G9
Method BLASTX
NCBI GI g422029
BLAST score 542
E value 2.0e-55
Match length 150
% identity 73
NCBI Description transcription factor OBF3.2, ocs element-binding - maize
>gi_297018_emb_CAA48904_ (X69152) ocs-element binding
factor 3.2 [Zea mays]

Seq. No. 400561
Seq. ID LIB3431-035-P1-K1-H1
Method BLASTX
NCBI GI g2407281
BLAST score 705
E value 1.0e-74
Match length 132
% identity 99
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]


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Seq. No.          400562
Seq. ID           LIB3431-035-P1-K1-H10
Method            BLASTX
NCBI GI           g132105
BLAST score       595
E value           9.0e-62
Match length      128
% identity        88
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

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Seq. No.      400563
Seq. ID       LIB3431-035-P1-K1-H11
Method        BLASTX
NCBI GI       g3914603
BLAST score    699
E value       5.0e-74
Match length  134
% identity    99
NCBI Description RIBULOSE BIPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                activase [Oryza sativa]
```

```
Seq. No.      400564
Seq. ID      LIB3431-035-P1-K1-H12
Method       BLASTX
NCBI GI      g6063542
BLAST score   351
E value      2.0e-33
Match length  109
% identity    72
NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of
the predicted gene.; similar to glyceraldehyde-3-phosphate
dehydrogenase. (M64118) [Oryza sativa]
```

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Seq. No.      400565
Seq. ID      LIB3431-035-P1-K1-H2
Method       BLASTX
NCBI GI      g1172813
BLAST score   563
E value      5.0e-58
Match length  108
% identity    99
NCBI Description  60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPPRESSOR SG12)
                >gi_1076752_pir_S49596 ribosomal protein L10.e, cytosolic
                - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor
                suppressor [Oryza sativa]
```

Seq. No. 400566

NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	400576
Seq. ID	LIB3431-035-P1-N1-C2
Method	BLASTX
NCBI GI	g482311
BLAST score	171
E value	4.0e-12
Match length	33
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	400577
Seq. ID	LIB3431-035-P1-N1-C3
Method	BLASTX
NCBI GI	g1362150
BLAST score	290
E value	1.0e-33
Match length	84
% identity	88
NCBI Description	hypothetical protein (clone AFN3) - wild oat (fragment) >gi_726478 (U20000) putative ORF1 [Avena fatua]
Seq. No.	400578
Seq. ID	LIB3431-035-P1-N1-C4
Method	BLASTN
NCBI GI	g2331130
BLAST score	227
E value	1.0e-125
Match length	251
% identity	98
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds
Seq. No.	400579
Seq. ID	LIB3431-035-P1-N1-C7
Method	BLASTN
NCBI GI	g218209
BLAST score	57
E value	3.0e-23
Match length	172
% identity	90
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106
Seq. No.	400580
Seq. ID	LIB3431-035-P1-N1-C8
Method	BLASTN
NCBI GI	g5042437
BLAST score	325
E value	0.0e+00
Match length	389
% identity	100

NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.	400581
Seq. ID	LIB3431-035-P1-N1-C9
Method	BLASTX
NCBI GI	g347451
BLAST score	237
E value	7.0e-20
Match length	47
% identity	98
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]
Seq. No.	400582
Seq. ID	LIB3431-035-P1-N1-D1
Method	BLASTX
NCBI GI	g1173347
BLAST score	190
E value	2.0e-14
Match length	41
% identity	95
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]
Seq. No.	400583
Seq. ID	LIB3431-035-P1-N1-D10
Method	BLASTX
NCBI GI	g82080
BLAST score	256
E value	3.0e-25
Match length	76
% identity	82
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]
Seq. No.	400584
Seq. ID	LIB3431-035-P1-N1-D11
Method	BLASTX
NCBI GI	g170131
BLAST score	152
E value	6.0e-10
Match length	47
% identity	66
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]
Seq. No.	400585
Seq. ID	LIB3431-035-P1-N1-D12
Method	BLASTN
NCBI GI	g2773153
BLAST score	364
E value	0.0e+00
Match length	388

Match length	94
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]
Seq. No.	400596
Seq. ID	LIB3431-035-P1-N1-E6
Method	BLASTX
NCBI GI	g115768
BLAST score	223
E value	4.0e-18
Match length	43
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_72743_pir_CDKV chlorophyll a/b-binding protein precursor - cucumber (fragment) >gi_167523 (M16057) chlorophyll a/b-binding protein [Cucumis sativus]
Seq. No.	400597
Seq. ID	LIB3431-035-P1-N1-E9
Method	BLASTX
NCBI GI	g2582822
BLAST score	362
E value	2.0e-34
Match length	79
% identity	85
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]
Seq. No.	400598
Seq. ID	LIB3431-035-P1-N1-F1
Method	BLASTX
NCBI GI	g671737
BLAST score	199
E value	2.0e-15
Match length	37
% identity	100
NCBI Description	(X74731) Chlorophyll a/b binding protein [Amaranthus hypochondriacus]
Seq. No.	400599
Seq. ID	LIB3431-035-P1-N1-F10
Method	BLASTX
NCBI GI	g115813
BLAST score	230
E value	6.0e-19
Match length	55
% identity	82
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.	400600
Seq. ID	LIB3431-035-P1-N1-F7

000T0T"9T049960

BLAST score 289
E value 6.0e-26
Match length 62
% identity 92
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 400606
Seq. ID LIB3431-035-P1-N1-G3
Method BLASTX
NCBI GI g2462750
BLAST score 184
E value 1.0e-13
Match length 53
% identity 68
NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 400607
Seq. ID LIB3431-035-P1-N1-G4
Method BLASTX
NCBI GI g1616659
BLAST score 343
E value 4.0e-32
Match length 75
% identity 88
NCBI Description (U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No. 400608
Seq. ID LIB3431-035-P1-N1-G8
Method BLASTN
NCBI GI g3885887
BLAST score 304
E value 1.0e-170
Match length 315
% identity 99
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 400609
Seq. ID LIB3431-035-P1-N1-H1
Method BLASTN
NCBI GI g218209
BLAST score 152
E value 7.0e-80
Match length 343
% identity 97
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 400610
Seq. ID LIB3431-035-P1-N1-H10
Method BLASTX
NCBI GI g347451
BLAST score 380
E value 2.0e-36

09684015-101000

Match length	69
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]
Seq. No.	400611
Seq. ID	LIB3431-035-P1-N1-H11
Method	BLASTN
NCBI GI	g3377792
BLAST score	263
E value	1.0e-146
Match length	334
% identity	95
NCBI Description	Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds
Seq. No.	400612
Seq. ID	LIB3431-035-P1-N1-H12
Method	BLASTN
NCBI GI	g6063530
BLAST score	364
E value	0.0e+00
Match length	389
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
Seq. No.	400613
Seq. ID	LIB3431-035-P1-N1-H2
Method	BLASTX
NCBI GI	g1172813
BLAST score	450
E value	1.0e-44
Match length	88
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPPRESSOR SG12) >gi_1076752_pir_S49596 ribosomal protein L10.e, cytosolic - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor supressor [Oryza sativa]
Seq. No.	400614
Seq. ID	LIB3431-035-P1-N1-H4
Method	BLASTX
NCBI GI	g417260
BLAST score	300
E value	3.0e-27
Match length	81
% identity	70
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]
Seq. No.	400615
Seq. ID	LIB3431-035-P1-N1-H5
Method	BLASTX
NCBI GI	g115813
BLAST score	171
E value	4.0e-12

Method	BLASTN
NCBI GI	g19094
BLAST score	52
E value	4.0e-20
Match length	64
% identity	95
NCBI Description	H.vulgare mRNA PsaN for photosystem I subunit N
Seq. No.	400626
Seq. ID	LIB3431-036-P1-K1-B3
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	400627
Seq. ID	LIB3431-036-P1-K1-B4
Method	BLASTX
NCBI GI	g2306981
BLAST score	385
E value	4.0e-37
Match length	68
% identity	99
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.	400628
Seq. ID	LIB3431-036-P1-K1-B5
Method	BLASTX
NCBI GI	g132105
BLAST score	567
E value	2.0e-58
Match length	122
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	400629
Seq. ID	LIB3431-036-P1-K1-B6
Method	BLASTX
NCBI GI	g4760553
BLAST score	703
E value	2.0e-74
Match length	142
% identity	96
NCBI Description	(AB019533) Nad-dependent formate dehydrogenase [Oryza

0984016 101000

```
Seq. No.      400631
Seq. ID      LIB3431-036-P1-K1-B9
Method       BLASTX
NCBI GI      g320618
BLAST score   486
E value      5.0e-49
Match length  111
% identity   84
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]
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Seq. No.      400633
Seq. ID      LIB3431-036-P1-K1-C11
Method       BLASTX
NCBI GI      g3126854
BLAST score   715
E value      7.0e-76
Match length  136
% identity    99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
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51321

0964016 303000

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Seq. No.          400645
Seq. ID           LIB3431-036-P1-K1-D5
Method            BLASTX
NCBI GI           g4519936
BLAST score       481
E value           2.0e-48
Match length      136
% identity        71
NCBI Description   (AB019186) RPR1 [Oryza sativa]
```

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Seq. No.      400647
Seq. ID      LIB3431-036-P1-K1-D7
Method       BLASTX
NCBI GI      g3789954
BLAST score   582
E value      3.0e-60
Match length  109
% identity    100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]
```

Seq. No.	400648
Seq. ID	LIB3431-036-P1-K1-D8
Method	BLASTX
NCBI GI	g3126854
BLAST score	662
E value	1.0e-69
Match length	124
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

51324

BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400660
 Seq. ID LIB3431-036-P1-K1-F12
 Method BLASTN
 NCBI GI g1245938
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
 heart atrium, mRNA, 2998 nt]

Seq. No. 400661
 Seq. ID LIB3431-036-P1-K1-F2
 Method BLASTX
 NCBI GI g6017100
 BLAST score 588
 E value 6.0e-61
 Match length 142
 % identity 71
 NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]

Seq. No. 400662
 Seq. ID LIB3431-036-P1-K1-F3
 Method BLASTX
 NCBI GI g131388
 BLAST score 383
 E value 6.0e-37
 Match length 127
 % identity 66
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
 SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
 THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
 photosystem II oxygen-evolving complex protein 1 - common
 wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
 33kDa oxygen evolving protein of photosystem II [Triticum
 aestivum]

Seq. No. 400663
 Seq. ID LIB3431-036-P1-K1-F4
 Method BLASTX
 NCBI GI g3789952
 BLAST score 275
 E value 3.0e-24
 Match length 55
 % identity 96
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
 sativa]

Seq. No. 400664

Seq. ID LIB3431-036-P1-K1-F6
 Method BLASTX
 NCBI GI g4558549
 BLAST score 627
 E value 2.0e-65
 Match length 144
 % identity 83
 NCBI Description (AC007138) putative SecA-type chloroplast protein transport factor [*Arabidopsis thaliana*]

Seq. No. 400665
 Seq. ID LIB3431-036-P1-K1-F7
 Method BLASTX
 NCBI GI g2191152
 BLAST score 149
 E value 2.0e-09
 Match length 105
 % identity 39
 NCBI Description (AF007269) A_IG002N01.31 gene product [*Arabidopsis thaliana*]

Seq. No. 400666
 Seq. ID LIB3431-036-P1-K1-F8
 Method BLASTX
 NCBI GI g2407281
 BLAST score 682
 E value 6.0e-72
 Match length 127
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza sativa*]

Seq. No. 400667
 Seq. ID LIB3431-036-P1-K1-G1
 Method BLASTX
 NCBI GI g2130052
 BLAST score 451
 E value 7.0e-45
 Match length 99
 % identity 89
 NCBI Description xylose isomerase (EC 5.3.1.5) - barley
 >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase
 [*Hordeum vulgare*]

Seq. No. 400668
 Seq. ID LIB3431-036-P1-K1-G10
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [*Oryza sativa*]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [*Oryza sativa*]

Seq. No. 400669

Seq. ID	LIB3431-036-P1-K1-G2
Method	BLASTX
NCBI GI	g3913808
BLAST score	590
E value	4.0e-61
Match length	132
% identity	89
NCBI Description	FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120) ferrochelatase [Oryza sativa]
Seq. No.	400670
Seq. ID	LIB3431-036-P1-K1-G4
Method	BLASTX
NCBI GI	g4079798
BLAST score	496
E value	4.0e-50
Match length	127
% identity	77
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]
Seq. No.	400671
Seq. ID	LIB3431-036-P1-K1-G5
Method	BLASTX
NCBI GI	g3126854
BLAST score	511
E value	6.0e-52
Match length	99
% identity	97
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	400672
Seq. ID	LIB3431-036-P1-K1-G6
Method	BLASTX
NCBI GI	g4895205
BLAST score	248
E value	4.0e-21
Match length	61
% identity	77
NCBI Description	(AC007661) putative alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	400673
Seq. ID	LIB3431-036-P1-K1-G7
Method	BLASTX
NCBI GI	g2695931
BLAST score	350
E value	5.0e-33
Match length	141
% identity	53
NCBI Description	(AJ222779) hypothetical protein [Hordeum vulgare]
Seq. No.	400674
Seq. ID	LIB3431-036-P1-K1-G8
Method	BLASTN
NCBI GI	g6015437

[Hordeum vulgare]

Seq. No. 400679
 Seq. ID LIB3431-036-P1-K1-H9
 Method BLASTX
 NCBI GI g1709846
 BLAST score 164
 E value 3.0e-11
 Match length 121
 % identity 44
 NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
 22 kDa component of photosystem II [Lycopersicon
 esculentum]

Seq. No. 400680
 Seq. ID LIB3431-036-P1-N1-A1
 Method BLASTN
 NCBI GI g576770
 BLAST score 280
 E value 1.0e-156
 Match length 304
 % identity 98
 NCBI Description Oryza sativa clone ST1 sucrose-regulated mRNA, 3'-end
 sequence

Seq. No. 400681
 Seq. ID LIB3431-036-P1-N1-A11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400682
 Seq. ID LIB3431-036-P1-N1-A4
 Method BLASTX
 NCBI GI g6103011
 BLAST score 515
 E value 2.0e-52
 Match length 115
 % identity 48
 NCBI Description (X84225) precursor of photosystem II subunit (22KDa)
 [Nicotiana tabacum]

Seq. No. 400683
 Seq. ID LIB3431-036-P1-N1-A5
 Method BLASTN
 NCBI GI g6016845
 BLAST score 206
 E value 1.0e-112
 Match length 347
 % identity 89
 NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400689
 Seq. ID LIB3431-036-P1-N1-B4
 Method BLASTX
 NCBI GI g2306981
 BLAST score 236
 E value 1.0e-19
 Match length 52
 % identity 87
 NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 400690
 Seq. ID LIB3431-036-P1-N1-B5
 Method BLASTX
 NCBI GI g132105
 BLAST score 443
 E value 7.0e-44
 Match length 80
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400691
 Seq. ID LIB3431-036-P1-N1-B6
 Method BLASTX
 NCBI GI g4760553
 BLAST score 429
 E value 3.0e-42
 Match length 82
 % identity 95
 NCBI Description (AB019533) Nad-dependent formate dehydrogenase [Oryza
 sativa]

Seq. No. 400692
 Seq. ID LIB3431-036-P1-N1-B7
 Method BLASTX
 NCBI GI g115794
 BLAST score 550
 E value 2.0e-56
 Match length 111
 % identity 94
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
 III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
 protein type III precursor (cab-13) - tomato

00684016.101000

% identity 92
 NCBI Description 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
 (BETA-KETOACYL-ACP SYNTHASE I) (KAS I)
 >gi_100555_pir_A39356 3-oxoacyl-[acyl-carrier-protein]
 synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
 - barley >gi_167065 (M60410) beta-ketoacyl-ACP synthase I
 [Hordeum vulgare]

Seq. No. 400698
 Seq. ID LIB3431-036-P1-N1-C9
 Method BLASTX
 NCBI GI g2511594
 BLAST score 326
 E value 4.0e-30
 Match length 95
 % identity 66
 NCBI Description (Y13694) multicatalytic endopeptidase complex, proteasome
 precursor, beta subunit [Arabidopsis thaliana]
 >gi_2827525_emb_CAA16533.1 (AL021633) multicatalytic
 endopeptidase complex, proteasome precursor, beta subunit
 [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
 proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No. 400699
 Seq. ID LIB3431-036-P1-N1-D1
 Method BLASTX
 NCBI GI g4105561
 BLAST score 391
 E value 9.0e-38
 Match length 85
 % identity 88
 NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No. 400700
 Seq. ID LIB3431-036-P1-N1-D10
 Method BLASTX
 NCBI GI g3036942
 BLAST score 363
 E value 2.0e-34
 Match length 71
 % identity 97
 NCBI Description (AB012636) light harvesting chlorophyll a/b-binding protein
 [Nicotiana glauca]

Seq. No. 400701
 Seq. ID LIB3431-036-P1-N1-D11
 Method BLASTX
 NCBI GI g482311
 BLAST score 428
 E value 4.0e-42
 Match length 86
 % identity 99
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
 (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
 complex protein 1 [Oryza sativa]

Seq. No. 400702

09584016-101000

% identity 66
NCBI Description (X97606) abscisic acid activated [Medicago sativa]

Seq. No. 400723
Seq. ID LIB3431-036-P1-N1-G7
Method BLASTX
NCBI GI g2695931
BLAST score 504
E value 5.0e-51
Match length 106
% identity 89
NCBI Description (AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No. 400724
Seq. ID LIB3431-036-P1-N1-G9
Method BLASTX
NCBI GI g6063542
BLAST score 390
E value 1.0e-37
Match length 71
% identity 100
NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 400725
Seq. ID LIB3431-036-P1-N1-H11
Method BLASTX
NCBI GI g115774
BLAST score 189
E value 4.0e-14
Match length 65
% identity 57
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE I CAB-13) (LHCP) >gi_72731_pir_CDPJ13 chlorophyll a/b-binding protein 13 precursor - petunia
>gi_20471_emb_CAA26210_(X02357) cab 13 precursor polypeptide (aa -33 to 233) [Petunia sp.]

Seq. No. 400726
Seq. ID LIB3431-036-P1-N1-H12
Method BLASTX
NCBI GI g552740
BLAST score 197
E value 2.0e-15
Match length 56
% identity 75
NCBI Description (M17841) ribosomal protein S7 [Zea mays]

Seq. No. 400727
Seq. ID LIB3431-036-P1-N1-H2
Method BLASTX
NCBI GI g6016428
BLAST score 301
E value 3.0e-27
Match length 63
% identity 83

E value 2.0e-09
 Match length 29
 % identity 90
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 400752
 Seq. ID LIB3431-037-P1-K1-C3
 Method BLASTX
 NCBI GI g5042409
 BLAST score 425
 E value 9.0e-42
 Match length 139
 % identity 61
 NCBI Description (AC006193) Putative membrane related protein [Arabidopsis thaliana]

Seq. No. 400753
 Seq. ID LIB3431-037-P1-K1-C4
 Method BLASTX
 NCBI GI g3776557
 BLAST score 389
 E value 1.0e-37
 Match length 142
 % identity 51
 NCBI Description (AC005388) Contains similarity to gi_2924495 hypothetical protein Rv1920 from Mycobacterium tuberculosis genome gb_AL022020. [Arabidopsis thaliana]

Seq. No. 400754
 Seq. ID LIB3431-037-P1-K1-C6
 Method BLASTX
 NCBI GI g3885892
 BLAST score 284
 E value 2.0e-35
 Match length 104
 % identity 72
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 400755
 Seq. ID LIB3431-037-P1-K1-C7
 Method BLASTX
 NCBI GI g5882720
 BLAST score 294
 E value 2.0e-26
 Match length 99
 % identity 60
 NCBI Description (AC008263) Similar to gb_D86180 phosphoribosylanthranilate transferase from Pisum sativum and contains 2 PF_00168 C2 (phospholipid binding) domains. ESTs gb_H76726, gb_T45544 and gb_N96377 come from this gene. [Arab

Seq. No. 400756
 Seq. ID LIB3431-037-P1-K1-C8
 Method BLASTX
 NCBI GI g3345477
 BLAST score 506
 E value 3.0e-51

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 400761
Seq. ID LIB3431-037-P1-K1-D5
Method BLASTX
NCBI GI g5734758
BLAST score 321
E value 1.0e-29
Match length 155
% identity 41
NCBI Description (AC007651) Similar to tuftelin-interacting protein
[Arabidopsis thaliana]

Seq. No. 400762
Seq. ID LIB3431-037-P1-K1-D6
Method BLASTX
NCBI GI g3335335
BLAST score 190
E value 3.0e-14
Match length 61
% identity 62
NCBI Description (AC004512) ESTs gb_F14113 and gb_T42122 come from this
region. [Arabidopsis thaliana]

Seq. No. 400763
Seq. ID LIB3431-037-P1-K1-D7
Method BLASTX
NCBI GI g3435096
BLAST score 273
E value 6.0e-24
Match length 101
% identity 55
NCBI Description (AF033587) SRZ21 [Arabidopsis thaliana]

Seq. No. 400764
Seq. ID LIB3431-037-P1-K1-E1
Method BLASTX
NCBI GI g1653513
BLAST score 158
E value 2.0e-10
Match length 81
% identity 41
NCBI Description (D90914) hypothetical protein [Synechocystis sp.]

Seq. No. 400765
Seq. ID LIB3431-037-P1-K1-E10
Method BLASTN
NCBI GI g6015437
BLAST score 35
E value 6.0e-10
Match length 35
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 400766
Seq. ID LIB3431-037-P1-K1-E11

Method BLASTX
 NCBI GI g132105
 BLAST score 748
 E value 1.0e-79
 Match length 157
 % identity 90
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400767
 Seq. ID LIB3431-037-P1-K1-E12
 Method BLASTX
 NCBI GI g3894193
 BLAST score 152
 E value 9.0e-10
 Match length 117
 % identity 38
 NCBI Description (AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No. 400768
 Seq. ID LIB3431-037-P1-K1-E2
 Method BLASTN
 NCBI GI g3075487
 BLAST score 59
 E value 2.0e-24
 Match length 187
 % identity 83
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 400769
 Seq. ID LIB3431-037-P1-K1-E3
 Method BLASTN
 NCBI GI g2239152
 BLAST score 290
 E value 1.0e-162
 Match length 306
 % identity 99
 NCBI Description O.sativa mRNA for putative T3/T7-like RNA polymerase, partial

Seq. No. 400770
 Seq. ID LIB3431-037-P1-K1-E5
 Method BLASTX
 NCBI GI g132105
 BLAST score 667
 E value 4.0e-70
 Match length 142
 % identity 89

NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 400771
Seq. ID LIB3431-037-P1-K1-E6
Method BLASTX
NCBI GI g132105
BLAST score 286
E value 2.0e-25
Match length 118
% identity 59

NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 400772
Seq. ID LIB3431-037-P1-K1-E7
Method BLASTX
NCBI GI g1076724
BLAST score 410
E value 5.0e-40
Match length 78
% identity 95

NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 400773
Seq. ID LIB3431-037-P1-K1-E8
Method BLASTX
NCBI GI g461999
BLAST score 708
E value 6.0e-75
Match length 154
% identity 90

NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No. 400774
Seq. ID LIB3431-037-P1-K1-E9
Method BLASTX
NCBI GI g118170
BLAST score 429
E value 3.0e-42
Match length 102

Seq. No. 400784
 Seq. ID LIB3431-037-P1-K1-F9
 Method BLASTX
 NCBI GI g417260
 BLAST score 421
 E value 3.0e-41
 Match length 128
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 400785
 Seq. ID LIB3431-037-P1-K1-G10
 Method BLASTX
 NCBI GI g2347098
 BLAST score 448
 E value 2.0e-44
 Match length 94
 % identity 86
 NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
 >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
 protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 400786
 Seq. ID LIB3431-037-P1-K1-G12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400787
 Seq. ID LIB3431-037-P1-K1-G2
 Method BLASTX
 NCBI GI g2501189
 BLAST score 520
 E value 6.0e-53
 Match length 138
 % identity 76
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
 >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 400788
 Seq. ID LIB3431-037-P1-K1-G3
 Method BLASTX
 NCBI GI g2565436
 BLAST score 159
 E value 1.0e-10
 Match length 99

% identity 39
 NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No. 400789
 Seq. ID LIB3431-037-P1-K1-G5
 Method BLASTX
 NCBI GI g1708191
 BLAST score 428
 E value 4.0e-42
 Match length 135
 % identity 55
 NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No. 400790
 Seq. ID LIB3431-037-P1-K1-G7
 Method BLASTX
 NCBI GI g548603
 BLAST score 698
 E value 2.0e-75
 Match length 148
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir_JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 400791
 Seq. ID LIB3431-037-P1-K1-G8
 Method BLASTX
 NCBI GI g3603401
 BLAST score 414
 E value 2.0e-40
 Match length 131
 % identity 61
 NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 400792
 Seq. ID LIB3431-037-P1-K1-G9
 Method BLASTX
 NCBI GI g320618
 BLAST score 546
 E value 6.0e-56
 Match length 123
 % identity 85
 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 400793
 Seq. ID LIB3431-037-P1-K1-H1
 Method BLASTX
 NCBI GI g3294467
 BLAST score 682
 E value 6.0e-72

NCBI Description	Rice complete chloroplast genome
Seq. No.	400803
Seq. ID	LIB3431-037-P1-N1-A4
Method	BLASTX
NCBI GI	g4996105
BLAST score	316
E value	5.0e-29
Match length	77
% identity	73
NCBI Description	(AB014076) histidine decarboxylase [Brassica napus]
Seq. No.	400804
Seq. ID	LIB3431-037-P1-N1-A5
Method	BLASTX
NCBI GI	g671740
BLAST score	336
E value	3.0e-31
Match length	84
% identity	80
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	400805
Seq. ID	LIB3431-037-P1-N1-A8
Method	BLASTX
NCBI GI	g167097
BLAST score	151
E value	7.0e-22
Match length	70
% identity	79
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]
Seq. No.	400806
Seq. ID	LIB3431-037-P1-N1-B1
Method	BLASTX
NCBI GI	g482311
BLAST score	320
E value	2.0e-29
Match length	64
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	400807
Seq. ID	LIB3431-037-P1-N1-B10
Method	BLASTX
NCBI GI	g132105
BLAST score	397
E value	2.0e-38
Match length	72
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

FBI LABORATORY

Seq. No.	400809
Seq. ID	LIB3431-037-P1-N1-B3
Method	BLASTN
NCBI GI	g3885891
BLAST score	262
E value	1.0e-145
Match length	330
% identity	95
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

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Seq. No.      400811
Seq. ID       LIB3431-037-P1-N1-C10
Method        BLASTX
NCBI GI       g2191138
BLAST score    253
E value       1.0e-21
Match length   73
% identity     70
NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis
                thaliana]
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51358

Match length	41
% identity	66
NCBI Description	(AC006193) Putative membrane related protein [Arabidopsis thaliana]
Seq. No.	400813
Seq. ID	LIB3431-037-P1-N1-C6
Method	BLASTX
NCBI GI	g3885892
BLAST score	471
E value	4.0e-47
Match length	89
% identity	100
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.	400814
Seq. ID	LIB3431-037-P1-N1-C8
Method	BLASTX
NCBI GI	g3345477
BLAST score	182
E value	2.0e-13
Match length	34
% identity	97
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.	400815
Seq. ID	LIB3431-037-P1-N1-C9
Method	BLASTX
NCBI GI	g3885886
BLAST score	199
E value	3.0e-15
Match length	35
% identity	100
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.	400816
Seq. ID	LIB3431-037-P1-N1-D1
Method	BLASTX
NCBI GI	g3789952
BLAST score	203
E value	1.0e-15
Match length	37
% identity	100
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]
Seq. No.	400817
Seq. ID	LIB3431-037-P1-N1-D10
Method	BLASTX
NCBI GI	g671740
BLAST score	263
E value	9.0e-23
Match length	51
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Match length 44
 % identity 75
 NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No. 400828
 Seq. ID LIB3431-037-P1-N1-F1
 Method BLASTX
 NCBI GI g2306981
 BLAST score 342
 E value 5.0e-32
 Match length 87
 % identity 72
 NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 400829
 Seq. ID LIB3431-037-P1-N1-F10
 Method BLASTX
 NCBI GI g2288969
 BLAST score 281
 E value 7.0e-25
 Match length 127
 % identity 47
 NCBI Description (Y12862) glutathione transferase [Zea mays]

Seq. No. 400830
 Seq. ID LIB3431-037-P1-N1-F11
 Method BLASTX
 NCBI GI g4469020
 BLAST score 258
 E value 3.0e-22
 Match length 59
 % identity 83
 NCBI Description (AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 400831
 Seq. ID LIB3431-037-P1-N1-F2
 Method BLASTN
 NCBI GI g20181
 BLAST score 87
 E value 4.0e-41
 Match length 167
 % identity 88
 NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No. 400832
 Seq. ID LIB3431-037-P1-N1-F3
 Method BLASTX
 NCBI GI g1706260
 BLAST score 442
 E value 9.0e-44
 Match length 82
 % identity 95
 NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
 cysteine proteinase 1 precursor - maize
 >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea

mays]

Seq. No. 400833
 Seq. ID LIB3431-037-P1-N1-F4
 Method BLASTX
 NCBI GI g128690
 BLAST score 533
 E value 2.0e-54
 Match length 120
 % identity 88
 NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
 >gi_66161_pir_DERZN3 NADH dehydrogenase (ubiquinone) (EC
 1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_
 (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
 >gi_226610_prf_1603356AG NADH dehydrogenase ND3 [Oryza
 sativa]

Seq. No. 400834
 Seq. ID LIB3431-037-P1-N1-F5
 Method BLASTX
 NCBI GI g131176
 BLAST score 333
 E value 6.0e-31
 Match length 65
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
 (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
 >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
 barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
 -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A
 10.8kD photosystem I protein [Hordeum vulgare var.
 distichum]

Seq. No. 400835
 Seq. ID LIB3431-037-P1-N1-F6
 Method BLASTX
 NCBI GI g548605
 BLAST score 277
 E value 2.0e-24
 Match length 59
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 400836
 Seq. ID LIB3431-037-P1-N1-F8
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

0964016 101000

Seq. No.	400838
Seq. ID	LIB3431-037-P1-N1-G1
Method	BLASTN
NCBI GI	g2950394
BLAST score	35
E value	5.0e-10
Match length	51
% identity	92
NCBI Description	Zea mays me gene, exons 1 to

```
Seq. No.      400840
Seq. ID      LIB3431-037-P1-N1-G12
Method       BLASTN
NCBI GI      g2072554
BLAST score   220
E value      1.0e-120
Match length 243
% identity   98
NCBI Description  Oryza sativa metallothionein-like protein mRNA, complete cds
```

51364

09664016101000

protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 400847
Seq. ID LIB3431-037-P1-N1-H1
Method BLASTX
NCBI GI g3294467
BLAST score 369
E value 3.0e-35
Match length 78
% identity 95
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]

Seq. No. 400848
Seq. ID LIB3431-037-P1-N1-H10
Method BLASTX
NCBI GI g517500
BLAST score 190
E value 5.0e-23
Match length 94
% identity 68
NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
protein [Zea mays] >gi_444338_prf_1906386A photosystem II
OE17 protein [Pisum sativum]

Seq. No. 400849
Seq. ID LIB3431-037-P1-N1-H11
Method BLASTX
NCBI GI g3126854
BLAST score 415
E value 1.0e-40
Match length 79
% identity 99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400850
Seq. ID LIB3431-037-P1-N1-H12
Method BLASTX
NCBI GI g733454
BLAST score 402
E value 3.0e-39
Match length 81
% identity 95
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 400851
Seq. ID LIB3431-037-P1-N1-H3
Method BLASTX
NCBI GI g482311
BLAST score 374
E value 8.0e-36
Match length 74
% identity 100
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
(strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 400852
 Seq. ID LIB3431-037-P1-N1-H4
 Method BLASTX
 NCBI GI g1708924
 BLAST score 252
 E value 2.0e-21
 Match length 54
 % identity 87
 NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
 MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate
 dehydrogenase (NADP+) [Vitis vinifera]

Seq. No. 400853
 Seq. ID LIB3431-037-P1-N1-H5
 Method BLASTX
 NCBI GI g671740
 BLAST score 202
 E value 1.0e-15
 Match length 38
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 400854
 Seq. ID LIB3431-037-P1-N1-H6
 Method BLASTX
 NCBI GI g4206195
 BLAST score 213
 E value 5.0e-17
 Match length 54
 % identity 67
 NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]
 >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein
 [Arabidopsis thaliana]

Seq. No. 400855
 Seq. ID LIB3431-037-P1-N1-H7
 Method BLASTX
 NCBI GI g548605
 BLAST score 493
 E value 8.0e-50
 Match length 109
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 400856
 Seq. ID LIB3431-037-P1-N1-H8
 Method BLASTX
 NCBI GI g3757515
 BLAST score 305
 E value 8.0e-28

Match length 73
 % identity 77
 NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]
 >gi_4581130_gb_AAD24620.1_AC005825_27 (AC005825)
 hypothetical protein [Arabidopsis thaliana]

Seq. No. 400857
 Seq. ID LIB3431-037-P1-N1-H9
 Method BLASTX
 NCBI GI g671740
 BLAST score 264
 E value 5.0e-23
 Match length 53
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 400858
 Seq. ID LIB3431-038-P1-K1-A1
 Method BLASTX
 NCBI GI g166410
 BLAST score 443
 E value 6.0e-44
 Match length 118
 % identity 71
 NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 400859
 Seq. ID LIB3431-038-P1-K1-A10
 Method BLASTX
 NCBI GI g3075488
 BLAST score 634
 E value 2.0e-66
 Match length 117
 % identity 100
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 400860
 Seq. ID LIB3431-038-P1-K1-A11
 Method BLASTX
 NCBI GI g3367596
 BLAST score 394
 E value 3.0e-38
 Match length 121
 % identity 59
 NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 400861
 Seq. ID LIB3431-038-P1-K1-A12
 Method BLASTX
 NCBI GI g729535
 BLAST score 223
 E value 4.0e-18
 Match length 76
 % identity 58
 NCBI Description FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)

095403 - 100000

Seq. No.	400863
Seq. ID	LIB3431-038-P1-K1-A3
Method	BLASTX
NCBI GI	g3548808
BLAST score	322
E value	8.0e-30
Match length	81
% identity	67
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

```
Seq. No.      400864
Seq. ID       LIB3431-038-P1-K1-A4
Method        BLASTX
NCBI GI       g5031281
BLAST score    274
E value       4.0e-24
Match length   71
% identity     75
NCBI Description (AF139499) unknown [Prunus armeniaca]
```

Seq. No.	400865
Seq. ID	LIB3431-038-P1-K1-A5
Method	BLASTX
NCBI GI	g2293480
BLAST score	431
E value	2.0e-42
Match length	85
% identity	98
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

```
Seq. No.          400866
Seq. ID           LIB3431-038-P1-K1-A7
Method            BLASTX
NCBI GI           g282882
BLAST score       175
E value           2.0e-12
Match length      105
% identity        37
NCBI Description   receptor-like protein kinase precursor - Arabidopsis
                   thaliana >gi_166848 (M84659) receptor-like protein kinase
                   [Arabidopsis thaliana]
```

51369

Method BLASTX
 NCBI GI g3822223
 BLAST score 444
 E value 4.0e-44
 Match length 123
 % identity 61
 NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1
 alpha subunit [Arabidopsis thaliana]

Seq. No. 400868
 Seq. ID LIB3431-038-P1-K1-B1
 Method BLASTX
 NCBI GI g2293480
 BLAST score 431
 E value 1.0e-42
 Match length 85
 % identity 98
 NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 400869
 Seq. ID LIB3431-038-P1-K1-B10
 Method BLASTX
 NCBI GI g4689384
 BLAST score 231
 E value 4.0e-19
 Match length 43
 % identity 100
 NCBI Description (AF139467) LHCII type I chlorophyll a/b binding protein
 [Vigna radiata]

Seq. No. 400870
 Seq. ID LIB3431-038-P1-K1-B11
 Method BLASTX
 NCBI GI g5734748
 BLAST score 206
 E value 4.0e-16
 Match length 129
 % identity 36
 NCBI Description (AC007651) Unknown protein [Arabidopsis thaliana]

Seq. No. 400871
 Seq. ID LIB3431-038-P1-K1-B3
 Method BLASTN
 NCBI GI g4959460
 BLAST score 35
 E value 5.0e-10
 Match length 35
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 400872
 Seq. ID LIB3431-038-P1-K1-B4
 Method BLASTX
 NCBI GI g2501190
 BLAST score 602
 E value 1.0e-62
 Match length 142

000101-91048950

% identity 85
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
>gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
- maize >gi_596080 (U17351) thiamine biosynthetic enzyme
[Zea mays]

Seq. No. 400873
Seq. ID LIB3431-038-P1-K1-B5
Method BLASTX
NCBI GI g448445
BLAST score 229
E value 7.0e-19
Match length 62
% identity 69
NCBI Description CF0 ATP synthase:SUBUNIT=9 [Spinacia oleracea]

Seq. No. 400874
Seq. ID LIB3431-038-P1-K1-B6
Method BLASTX
NCBI GI g710308
BLAST score 732
E value 8.0e-78
Match length 143
% identity 97
NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 400875
Seq. ID LIB3431-038-P1-K1-B7
Method BLASTX
NCBI GI g400879
BLAST score 383
E value 6.0e-37
Match length 135
% identity 60
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
(PSI-N) >gi_479690_pir_S35159 photosystem I chain psaN -
barley >gi_19095_emb_CAA47056_ (X66428) photosystem I
subunit N [Hordeum vulgare]

Seq. No. 400876
Seq. ID LIB3431-038-P1-K1-B8
Method BLASTX
NCBI GI g4115918
BLAST score 213
E value 6.0e-17
Match length 50
% identity 82
NCBI Description (AF118222) similar to nascent polypeptide associated
complex alpha chain [Arabidopsis thaliana]

Seq. No. 400877
Seq. ID LIB3431-038-P1-K1-B9
Method BLASTX
NCBI GI g132105
BLAST score 759
E value 5.0e-81
Match length 139

% identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400878
 Seq. ID LIB3431-038-P1-K1-C10
 Method BLASTX
 NCBI GI g167097
 BLAST score 188
 E value 9.0e-27
 Match length 76
 % identity 82
 NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
 [Hordeum vulgare]

Seq. No. 400879
 Seq. ID LIB3431-038-P1-K1-C11
 Method BLASTX
 NCBI GI g4204263
 BLAST score 349
 E value 6.0e-33
 Match length 113
 % identity 60
 NCBI Description (AC005223) 40409 [Arabidopsis thaliana]

Seq. No. 400880
 Seq. ID LIB3431-038-P1-K1-C12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 8.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400881
 Seq. ID LIB3431-038-P1-K1-C2
 Method BLASTX
 NCBI GI g320618
 BLAST score 333
 E value 4.0e-31
 Match length 92
 % identity 74
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

NCBI GI g4056488
 BLAST score 477
 E value 6.0e-48
 Match length 105
 % identity 76
 NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 400888
 Seq. ID LIB3431-038-P1-K1-D10
 Method BLASTN
 NCBI GI g3063523
 BLAST score 50
 E value 6.0e-19
 Match length 138
 % identity 84
 NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 400889
 Seq. ID LIB3431-038-P1-K1-D11
 Method BLASTX
 NCBI GI g3075488
 BLAST score 483
 E value 1.0e-48
 Match length 93
 % identity 100
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 400890
 Seq. ID LIB3431-038-P1-K1-D12
 Method BLASTX
 NCBI GI g132105
 BLAST score 552
 E value 9.0e-57
 Match length 117
 % identity 90
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400891
 Seq. ID LIB3431-038-P1-K1-D2
 Method BLASTX
 NCBI GI g3914587
 BLAST score 254
 E value 9.0e-22
 Match length 112
 % identity 50
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_1076711_pir_S49992 ribulose-1,5-bisphosphate carboxylase/oxygenase - Aegilops

000001-91018950

squarrosa >gi_599620_emb_CAA58150_ (X83095) rbcS gene
[Aegilops squarrosa]

Seq. No. 400892
Seq. ID LIB3431-038-P1-K1-D5
Method BLASTX
NCBI GI g131225
BLAST score 586
E value 1.0e-60
Match length 144
% identity 78
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 400893
Seq. ID LIB3431-038-P1-K1-D7
Method BLASTX
NCBI GI g4582445
BLAST score 269
E value 2.0e-23
Match length 64
% identity 70
NCBI Description (AC007071) unknown protein [Arabidopsis thaliana]
>gi_4589952_gb_AAD26470.1 AC007169_2 (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No. 400894
Seq. ID LIB3431-038-P1-K1-D9
Method BLASTX
NCBI GI g2760334
BLAST score 294
E value 2.0e-26
Match length 76
% identity 64
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]

Seq. No. 400895
Seq. ID LIB3431-038-P1-K1-E1
Method BLASTX
NCBI GI g1001532
BLAST score 251
E value 2.0e-21
Match length 93
% identity 52
NCBI Description (D64000) hypothetical protein [Synechocystis sp.]

Seq. No. 400896
Seq. ID LIB3431-038-P1-K1-E10
Method BLASTX
NCBI GI g82080
BLAST score 638
E value 8.0e-67
Match length 140
% identity 81
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

0964016101000

```
Seq. No.      400905
Seq. ID      LIB3431-038-P1-K1-F11
Method       BLASTX
NCBI GI      g132105
BLAST score   322
E value      4.0e-46
Match length  110
% identity    87
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

```
sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]
```

```
Seq. No.      400906
Seq. ID      LIB3431-038-P1-K1-F2
Method       BLASTN
NCBI GI      g6015437
BLAST score   35
E value      5.0e-10
Match length  35
% identity    100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.      400907
Seq. ID      LIB3431-038-P1-K1-F3
Method       BLASTX
NCBI GI      g2497903
BLAST score   220
E value      8.0e-18
Match length  59
% identity    68
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2
                >gi_1752831_dbj_BAA14038.1_(D89931) metallothionein-like
                protein [Oryza sativa] >gi_1815628 (U43530)
                metallothionein-like type 2 [Oryza sativa]
```

Seq. No.	400908
Seq. ID	LIB3431-038-P1-K1-F4
Method	BLASTX
NCBI GI	g3928097
BLAST score	213
E value	6.0e-17
Match length	94
% identity	47
NCBI Description	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	400909
Seq. ID	LIB3431-038-P1-K1-F5
Method	BLASTX
NCBI GI	g2407281
BLAST score	653
E value	1.0e-68
Match length	127
% identity	94
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

```
Seq. No.      400910
Seq. ID       LIB3431-038-P1-K1-F6
Method        BLASTX
NCBI GI       g548603
BLAST score   407
E value       1.0e-39
Match length  118
% identity    71
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
```


09634016 103000

```
Seq. No.      400917
Seq. ID      LIB3431-038-P1-K1-G8
Method       BLASTX
NCBI GI      g733454
BLAST score   604
E value      8.0e-63
Match length  138
% identity    83
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
```

```
Seq. No.      400919
Seq. ID      LIB3431-038-P1-K1-H11
Method       BLASTX
NCBI GI      g1170937
BLAST score   760
E value      4.0e-81
Match length  144
% identity    100
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_(Z26867) S-adenosyl methionine
synthetase [Oryza sativa]
```

51380

09684016-101000

Seq. ID LIB3431-038-P1-K1-H6
 Method BLASTX
 NCBI GI g132105
 BLAST score 591
 E value 3.0e-61
 Match length 127
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400926
 Seq. ID LIB3431-038-P1-K1-H7
 Method BLASTN
 NCBI GI g1245938
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No. 400927
 Seq. ID LIB3431-038-P1-K1-H8
 Method BLASTX
 NCBI GI g5007084
 BLAST score 729
 E value 2.0e-77
 Match length 137
 % identity 100
 NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]

Seq. No. 400928
 Seq. ID LIB3431-038-P1-K1-H9
 Method BLASTX
 NCBI GI g6006363
 BLAST score 267
 E value 3.0e-23
 Match length 50
 % identity 100
 NCBI Description (AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No. 400929
 Seq. ID LIB3431-038-P1-N1-A10
 Method BLASTX
 NCBI GI g3153151
 BLAST score 162
 E value 5.0e-11

0669+016 = J0670.0-0158

```
Seq. No.      400936
Seq. ID      LIB3431-038-P1-N1-B1
Method       BLASTN
NCBI GI      g2331130
BLAST score   187
E value      1.0e-101
Match length 235
% identity   95
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds
```

```
Seq. No.      400937
Seq. ID      LIB3431-038-P1-N1-B10
Method       BLASTX
NCBI GI      g4689384
BLAST score   231
E value      4.0e-19
Match length  43
% identity    100
NCBI Description (AF139467) LHCII type I chlorophyll a/b binding protein
               [Vigna radiata]
```

```
Seq. No.      400938
Seq. ID      LIB3431-038-P1-N1-B3
Method       BLASTX
NCBI GI      g3192019
BLAST score   146
E value      4.0e-09
Match length  50
% identity   52
NCBI Description (AL023797) uridylyate kinase [Streptomyces coelicolor]
```

```
Seq. No.      400939
Seq. ID      LIB3431-038-P1-N1-B4
Method       BLASTX
NCBI GI      g2501190
BLAST score   155
E value      4.0e-10
Match length  51
% identity    69
NCBI Description  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
                - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                [Zea mays]
```

Seq. No. 400940
 Seq. ID LIB3431-038-P1-N1-B5
 Method BLASTX
 NCBI GI g461595
 BLAST score 188
 E value 5.0e-14
 Match length 98
 % identity 44
 NCBI Description ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
 >gi_479533_pir_S34473 H+-transporting ATP synthase (EC
 3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520
 (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]

Seq. No. 400941
 Seq. ID LIB3431-038-P1-N1-B6
 Method BLASTX
 NCBI GI g710308
 BLAST score 338
 E value 1.0e-31
 Match length 63
 % identity 95
 NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 400942
 Seq. ID LIB3431-038-P1-N1-B8
 Method BLASTX
 NCBI GI g1658271
 BLAST score 147
 E value 2.0e-09
 Match length 40
 % identity 78
 NCBI Description (U74622) nascent polypeptide associated complex alpha chain
 [Nicotiana tabacum]

Seq. No. 400943
 Seq. ID LIB3431-038-P1-N1-B9
 Method BLASTX
 NCBI GI g132105
 BLAST score 354
 E value 2.0e-33
 Match length 65
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400944
 Seq. ID LIB3431-038-P1-N1-C1
 Method BLASTN
 NCBI GI g11957

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 400955
 Seq. ID LIB3431-038-P1-N1-D12
 Method BLASTX
 NCBI GI g347451
 BLAST score 197
 E value 4.0e-15
 Match length 62
 % identity 63
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 400956
 Seq. ID LIB3431-038-P1-N1-D2
 Method BLASTX
 NCBI GI g347451
 BLAST score 208
 E value 2.0e-16
 Match length 48
 % identity 85
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 400957
 Seq. ID LIB3431-038-P1-N1-D5
 Method BLASTX
 NCBI GI g131225
 BLAST score 311
 E value 2.0e-28
 Match length 81
 % identity 75
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 400958
 Seq. ID LIB3431-038-P1-N1-D7
 Method BLASTX
 NCBI GI g4582445
 BLAST score 269
 E value 1.0e-23
 Match length 64
 % identity 70
 NCBI Description (AC007071) unknown protein [Arabidopsis thaliana]
 >gi_4589952_gb_AAD26470.1 AC007169_2 (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No. 400959
 Seq. ID LIB3431-038-P1-N1-E10
 Method BLASTX
 NCBI GI g115813
 BLAST score 248
 E value 4.0e-21
 Match length 56
 % identity 86

% identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 400970
 Seq. ID LIB3431-038-P1-N1-F6
 Method BLASTX
 NCBI GI g548603
 BLAST score 535
 E value 1.0e-54
 Match length 109
 % identity 94
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir_JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 400971
 Seq. ID LIB3431-038-P1-N1-G1
 Method BLASTX
 NCBI GI g1362150
 BLAST score 388
 E value 2.0e-37
 Match length 81
 % identity 89
 NCBI Description hypothetical protein (clone AFN3) - wild oat (fragment) >gi_726478 (U20000) putative ORF1 [Avena fatua]

Seq. No. 400972
 Seq. ID LIB3431-038-P1-N1-G11
 Method BLASTN
 NCBI GI g5734616
 BLAST score 397
 E value 0.0e+00
 Match length 409
 % identity 99
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No. 400973
 Seq. ID LIB3431-038-P1-N1-G12
 Method BLASTX
 NCBI GI g132105
 BLAST score 315
 E value 6.0e-29
 Match length 60
 % identity 98
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400974

0563016 101000

Seq. No.	400990
Seq. ID	LIB3431-039-P1-K2-B11
Method	BLASTN
NCBI GI	g11957
BLAST score	127
E value	4.0e-65
Match length	251
% identity	88
NCBI Description	Rice complete chloroplast genome

```
Seq. No.      400992
Seq. ID      LIB3431-039-P1-K2-B3
Method       BLASTX
NCBI GI      g733454
BLAST score   483
E value      9.0e-49
Match length  111
% identity    82
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
```

```
Seq. No.      400993
Seq. ID      LIB3431-039-P1-K2-B6
Method       BLASTX
NCBI GI      g3126854
BLAST score   149
E value      7.0e-10
Match length  30
% identity    100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      400994
Seq. ID       LIB3431-039-P1-K2-B7
Method        BLASTX
NCBI GI       g3345477
BLAST score   626
E value       2.0e-65
Match length  120
% identity    99
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

```
Seq. No.      400995
Seq. ID      LIB3431-039-P1-K2-B8
Method       BLASTX
NCBI GI      g131166
BLAST score   503
E value      3.0e-51
Match length  97
% identity    96
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_82100_pir_S00449
                  photosystem I chain II precursor - tomato >gi_170492
                  (M21344) photosystem I subunit II protein precursor
                  [Lycopersicon esculentum] >gi_226544_prf_1601516A
                  photosystem I reaction center II [Lycopersicon esculentum]
```

```
Seq. No.      400996
Seq. ID      LIB3431-039-P1-K2-C1
Method       BLASTX
NCBI GI      g541950
BLAST score   237
E value      8.0e-20
Match length  69
% identity   67
NCBI Description SPCP1 protein - soybean >gi_310576 (L12257).nodulin-26
               [Glycine max]
```

```
Seq. No.      400997
Seq. ID      LIB3431-039-P1-K2-C10
Method       BLASTX
NCBI GI      g289920
BLAST score   238
E value      5.0e-20
Match length  44
% identity    100
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
                hirsutum]
```

Seq. No.	400998
Seq. ID	LIB3431-039-P1-K2-C3
Method	BLASTX
NCBI GI	g3868758
BLAST score	612
E value	8.0e-64
Match length	114
% identity	96
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 400999
 Seq. ID LIB3431-039-P1-K2-C4
 Method BLASTX
 NCBI GI g1706260
 BLAST score 363
 E value 6.0e-35
 Match length 81
 % identity 85
 NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
 cysteine proteinase 1 precursor - maize
 >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
 mays]

Seq. No. 401000
 Seq. ID LIB3431-039-P1-K2-C5
 Method BLASTX
 NCBI GI g3126854
 BLAST score 772
 E value 2.0e-82
 Match length 144
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401001
 Seq. ID LIB3431-039-P1-K2-C6
 Method BLASTX
 NCBI GI g320618
 BLAST score 464
 E value 2.0e-46
 Match length 107
 % identity 82
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401002
 Seq. ID LIB3431-039-P1-K2-C7
 Method BLASTN
 NCBI GI g6015437
 BLAST score 37
 E value 2.0e-11
 Match length 48
 % identity 66
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 401003
 Seq. ID LIB3431-039-P1-K2-C8
 Method BLASTX
 NCBI GI g733454
 BLAST score 369
 E value 2.0e-35
 Match length 100
 % identity 71
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
 [Zea mays]

Seq. No. 401004
 Seq. ID LIB3431-039-P1-K2-C9
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 7.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 401005
 Seq. ID LIB3431-039-P1-K2-D10
 Method BLASTX
 NCBI GI g131225
 BLAST score 386
 E value 1.0e-37
 Match length 83
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 401006
 Seq. ID LIB3431-039-P1-K2-D3
 Method BLASTX
 NCBI GI g347451
 BLAST score 225
 E value 2.0e-18
 Match length 43
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
 sativa]

Seq. No. 401007
 Seq. ID LIB3431-039-P1-K2-D4
 Method BLASTX
 NCBI GI g4680193
 BLAST score 226
 E value 4.0e-19
 Match length 60
 % identity 63
 NCBI Description (AF111710) putative farnesyl pyrophosphate synthase [Oryza
 sativa subsp. indica]

Seq. No. 401008
 Seq. ID LIB3431-039-P1-K2-D6
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 5.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

000T0T"9T04B960

BLAST score	287
E value	1.0e-25
Match length	56
% identity	96
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_169663 (M81885) S-adenosylhomocysteine hydrolase [Petroselinum crispum]
Seq. No.	401038
Seq. ID	LIB3431-039-P1-N1-A6
Method	BLASTX
NCBI GI	g1835731
BLAST score	403
E value	3.0e-39
Match length	89
% identity	88
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.	401039
Seq. ID	LIB3431-039-P1-N1-A7
Method	BLASTX
NCBI GI	g3808101
BLAST score	350
E value	5.0e-33
Match length	80
% identity	90
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.	401040
Seq. ID	LIB3431-039-P1-N1-A9
Method	BLASTX
NCBI GI	g1707008
BLAST score	384
E value	4.0e-37
Match length	92
% identity	78
NCBI Description	(U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]
Seq. No.	401041
Seq. ID	LIB3431-039-P1-N1-B10
Method	BLASTN
NCBI GI	g11957
BLAST score	256
E value	1.0e-142
Match length	464
% identity	97
NCBI Description	Rice complete chloroplast genome
Seq. No.	401042
Seq. ID	LIB3431-039-P1-N1-B2
Method	BLASTX
NCBI GI	g3036951
BLAST score	333
E value	4.0e-31
Match length	64
% identity	100

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
[Nicotiana sylvestris]

Seq. No. 401043
Seq. ID LIB3431-039-P1-N1-B3
Method BLASTX
NCBI GI g733454
BLAST score 383
E value 6.0e-37
Match length 78
% identity 95

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 401044
Seq. ID LIB3431-039-P1-N1-B5
Method BLASTX
NCBI GI g113170
BLAST score 239
E value 5.0e-20
Match length 66
% identity 71

NCBI Description ACYL CARRIER PROTEIN II PRECURSOR (ACP II)
>gi_99531_pir_S12310 acyl carrier protein II - spinach
>gi_21232_emb_CAA36288_ (X52065) acyl carrier protein II
[Spinacia oleracea]

Seq. No. 401045
Seq. ID LIB3431-039-P1-N1-B6
Method BLASTX
NCBI GI g3126854
BLAST score 345
E value 2.0e-32
Match length 65
% identity 100

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401046
Seq. ID LIB3431-039-P1-N1-B7
Method BLASTX
NCBI GI g3345477
BLAST score 226
E value 2.0e-18
Match length 42
% identity 100

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401047
Seq. ID LIB3431-039-P1-N1-B8
Method BLASTN
NCBI GI g167084
BLAST score 35
E value 3.0e-10
Match length 47
% identity 94

NCBI Description Barley PSI-D subunit of photosystem I (PsaD) mRNA, complete
cds

Seq. No. 401048
 Seq. ID LIB3431-039-P1-N1-C1
 Method BLASTX
 NCBI GI g541951
 BLAST score 421
 E value 2.0e-41
 Match length 95
 % identity 80
 NCBI Description SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
 [Glycine max]

Seq. No. 401049
 Seq. ID LIB3431-039-P1-N1-C10
 Method BLASTX
 NCBI GI g289920
 BLAST score 177
 E value 7.0e-13
 Match length 34
 % identity 94
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
 hirsutum]

Seq. No. 401050
 Seq. ID LIB3431-039-P1-N1-C11
 Method BLASTX
 NCBI GI g2911043
 BLAST score 143
 E value 9.0e-09
 Match length 59
 % identity 47
 NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 401051
 Seq. ID LIB3431-039-P1-N1-C3
 Method BLASTX
 NCBI GI g3868758
 BLAST score 552
 E value 1.0e-56
 Match length 112
 % identity 91
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 401052
 Seq. ID LIB3431-039-P1-N1-C4
 Method BLASTX
 NCBI GI g1706260
 BLAST score 349
 E value 7.0e-33
 Match length 67
 % identity 94
 NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
 cysteine proteinase 1 precursor - maize
 >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
 mays]

Seq. No. 401053

09684016-101000

Seq. ID LIB3431-039-P1-N1-C5
Method BLASTX
NCBI GI g3126854
BLAST score 299
E value 5.0e-27
Match length 58
% identity 98
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401054
Seq. ID LIB3431-039-P1-N1-C6
Method BLASTX
NCBI GI g3036946
BLAST score 313
E value 8.0e-29
Match length 61
% identity 98
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 401055
Seq. ID LIB3431-039-P1-N1-C8
Method BLASTN
NCBI GI g2073379
BLAST score 71
E value 1.0e-31
Match length 139
% identity 86
NCBI Description Rice CP26 mRNA, partial sequence

Seq. No. 401056
Seq. ID LIB3431-039-P1-N1-C9
Method BLASTN
NCBI GI g2072554
BLAST score 277
E value 1.0e-154
Match length 341
% identity 95
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401057
Seq. ID LIB3431-039-P1-N1-D3
Method BLASTN
NCBI GI g218209
BLAST score 48
E value 8.0e-18
Match length 68
% identity 93
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 401058
Seq. ID LIB3431-039-P1-N1-D4
Method BLASTX
NCBI GI g4115416

% identity 93
 NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein
 [Vigna radiata]

Seq. No. 401064
 Seq. ID LIB3431-039-P1-N1-E7
 Method BLASTX
 NCBI GI g671740
 BLAST score 433
 E value 9.0e-43
 Match length 78
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 401065
 Seq. ID LIB3431-039-P1-N1-F3
 Method BLASTX
 NCBI GI g464980
 BLAST score 415
 E value 1.0e-40
 Match length 80
 % identity 96
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_166422 (L06967)
 ubiquitin carrier protein [Medicago sativa]

Seq. No. 401066
 Seq. ID LIB3431-039-P1-N1-F6
 Method BLASTX
 NCBI GI g2598589
 BLAST score 234
 E value 2.0e-19
 Match length 70
 % identity 60
 NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 401067
 Seq. ID LIB3431-039-P1-N1-F7
 Method BLASTX
 NCBI GI g5729704
 BLAST score 249
 E value 3.0e-21
 Match length 102
 % identity 45
 NCBI Description (AC007927) unknown protein, 5' partial [Arabidopsis
 thaliana]

Seq. No. 401068
 Seq. ID LIB3431-039-P1-N1-F8
 Method BLASTN
 NCBI GI g2570514
 BLAST score 287
 E value 1.0e-160
 Match length 335
 % identity 96
 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	401069
Seq. ID	LIB3431-039-P1-N1-F9
Method	BLASTN
NCBI GI	g2073379
BLAST score	168
E value	2.0e-89
Match length	243
% identity	92
NCBI Description	Rice CP26 mRNA, partial sequence
Seq. No.	401070
Seq. ID	LIB3431-039-P1-N1-G1
Method	BLASTX
NCBI GI	g1168587
BLAST score	200
E value	2.0e-15
Match length	45
% identity	87
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_1084467_pir_S43728 H+-transporting ATP synthase (EC 3.6.1.34) - sorghum >gi_311231_emb_CAA46803_ (X66004) H(+)-transporting ATP synthase [Sorghum bicolor]
Seq. No.	401071
Seq. ID	LIB3431-039-P1-N1-G10
Method	BLASTX
NCBI GI	g1296955
BLAST score	396
E value	2.0e-38
Match length	76
% identity	45
NCBI Description	(X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.	401072
Seq. ID	LIB3431-039-P1-N1-G11
Method	BLASTX
NCBI GI	g1296955
BLAST score	320
E value	2.0e-29
Match length	73
% identity	39
NCBI Description	(X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.	401073
Seq. ID	LIB3431-039-P1-N1-G12
Method	BLASTX
NCBI GI	g115813
BLAST score	257
E value	4.0e-22
Match length	61
% identity	82
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.	401074

BLAST score 409
 E value 6.0e-40
 Match length 77
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401079
 Seq. ID LIB3431-039-P1-N1-G7
 Method BLASTX
 NCBI GI g4206765
 BLAST score 180
 E value 5.0e-13
 Match length 77
 % identity 52
 NCBI Description (AF104329) putative type 1 membrane protein [Arabidopsis thaliana]

Seq. No. 401080
 Seq. ID LIB3431-039-P1-N1-G8
 Method BLASTX
 NCBI GI g2464852
 BLAST score 171
 E value 5.0e-12
 Match length 80
 % identity 49
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 401081
 Seq. ID LIB3431-039-P1-N1-H3
 Method BLASTX
 NCBI GI g1708424
 BLAST score 267
 E value 3.0e-23
 Match length 61
 % identity 74
 NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

Seq. No. 401082
 Seq. ID LIB3431-039-P1-N1-H6
 Method BLASTX
 NCBI GI g671740
 BLAST score 380
 E value 2.0e-36
 Match length 69
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401083
 Seq. ID LIB3431-039-P1-N1-H8
 Method BLASTX
 NCBI GI g3738261

sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 401093
Seq. ID LIB3431-040-P1-K2-B7
Method BLASTX
NCBI GI g1353352
BLAST score 302
E value 2.0e-27
Match length 94
% identity 66
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
reinhardtii]

Seq. No. 401094
Seq. ID LIB3431-040-P1-K2-C1
Method BLASTX
NCBI GI g114521
BLAST score 520
E value 6.0e-53
Match length 127
% identity 86
NCBI Description ATP SYNTHASE ALPHA CHAIN >gi_67827_pir_PWRZA
H+-transporting ATP synthase (EC 3.6.1.34) alpha chain -
rice chloroplast >gi_11979_emb_CAA33993_ (X15901) ATPase
alpha subunit [Oryza sativa] >gi_226696_prf_1603356X
ATPase alpha [Oryza sativa]

Seq. No. 401095
Seq. ID LIB3431-040-P1-K2-C11
Method BLASTX
NCBI GI g3126854
BLAST score 520
E value 7.0e-53
Match length 104
% identity 96
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401096
Seq. ID LIB3431-040-P1-K2-C12
Method BLASTX
NCBI GI g231610
BLAST score 193
E value 5.0e-15
Match length 54
% identity 65
NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
>gi_67880_pir_PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase
(gamma subunit) [Nicotiana tabacum]

Seq. No. 401097
Seq. ID LIB3431-040-P1-K2-C2
Method BLASTN
NCBI GI g218207
BLAST score 165

E value	1.0e-87
Match length	253
% identity	91
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

```
Seq. No.      401098
Seq. ID      LIB3431-040-P1-K2-C3
Method       BLASTX
NCBI GI      g2130042
BLAST score   486
E value      6.0e-56
Match length  126
% identity    92
NCBI Description  Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916)
                protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                vulgare]
```

Seq. No.	401099
Seq. ID	LIB3431-040-P1-K2-C4
Method	BLASTN
NCBI GI	g5295936
BLAST score	36
E value	3.0e-11
Match length	48
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

```
Seq. No.          401100
Seq. ID           LIB3431-040-P1-K2-C5
Method            BLASTX
NCBI GI           g3559814
BLAST score       658
E value           4.0e-69
Match length      146
% identity        86
NCBI Description   (Y15781) transketolase 1 [Capsicum annuum]
```

```
Seq. No.      401101
Seq. ID      LIB3431-040-P1-K2-C6
Method       BLASTX
NCBI GI      g2501356
BLAST score   523
E value      3.0e-53
Match length  139
% identity    74
NCBI Description  TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
                >gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor
                [Solanum tuberosum]
```

```
Seq. No.      401102
Seq. ID      LIB3431-040-P1-K2-C7
Method       BLASTX
NCBI GI      g4995921
BLAST score  230
```


NCBI GI g4490317
 BLAST score 319
 E value 3.0e-29
 Match length 158
 % identity 42
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 401113
 Seq. ID LIB3431-040-P1-K2-E12
 Method BLASTX
 NCBI GI g729668
 BLAST score 228
 E value 1.0e-18
 Match length 66
 % identity 61
 NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1,
 drought-inducible - Lycopersicon pennellii >gi_436823
 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 401114
 Seq. ID LIB3431-040-P1-K2-E2
 Method BLASTX
 NCBI GI g120661
 BLAST score 198
 E value 1.0e-16
 Match length 90
 % identity 60
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
 PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
 dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 401115
 Seq. ID LIB3431-040-P1-K2-E3
 Method BLASTX
 NCBI GI g132105
 BLAST score 503
 E value 3.0e-51
 Match length 104
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401116
 Seq. ID LIB3431-040-P1-K2-E4
 Method BLASTX
 NCBI GI g2407281
 BLAST score 254
 E value 3.0e-22
 Match length 68
 % identity 75

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 401117
Seq. ID LIB3431-040-P1-K2-E5
Method BLASTN
NCBI GI g3819221
BLAST score 84
E value 3.0e-39
Match length 282
% identity 83
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0721

Seq. No. 401118
Seq. ID LIB3431-040-P1-K2-E8
Method BLASTX
NCBI GI g2407281
BLAST score 455
E value 2.0e-45
Match length 119
% identity 77
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 401119
Seq. ID LIB3431-040-P1-K2-E9
Method BLASTX
NCBI GI g1174745
BLAST score 359
E value 3.0e-34
Match length 80
% identity 89
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
>gi_1363523_pir_S53761 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - rye
>gi_609262_emb_CAA83533_(Z32521) triosephosphate isomerase [Secale cereale] >gi_1095494_prf_2109226B triosephosphate isomerase [Secale cereale]

Seq. No. 401120
Seq. ID LIB3431-040-P1-K2-F10
Method BLASTX
NCBI GI g3885894
BLAST score 507
E value 2.0e-51
Match length 132
% identity 77
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 401121
Seq. ID LIB3431-040-P1-K2-F11
Method BLASTX
NCBI GI g2104959
BLAST score 324
E value 2.0e-30
Match length 77
% identity 74

Match length 142
 % identity 56
 NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 401132
 Seq. ID LIB3431-040-P1-K2-G8
 Method BLASTX
 NCBI GI g3080420
 BLAST score 389
 E value 1.0e-37
 Match length 120
 % identity 62
 NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 401133
 Seq. ID LIB3431-040-P1-K2-H10
 Method BLASTN
 NCBI GI g6103440
 BLAST score 93
 E value 5.0e-45
 Match length 149
 % identity 91
 NCBI Description Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds

Seq. No. 401134
 Seq. ID LIB3431-040-P1-K2-H12
 Method BLASTN
 NCBI GI g2072554
 BLAST score 146
 E value 3.0e-76
 Match length 186
 % identity 95
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401135
 Seq. ID LIB3431-040-P1-K2-H2
 Method BLASTN
 NCBI GI g3135542
 BLAST score 39
 E value 8.0e-13
 Match length 67
 % identity 90
 NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds

Seq. No. 401136
 Seq. ID LIB3431-040-P1-K2-H5
 Method BLASTX
 NCBI GI g4584342
 BLAST score 221
 E value 6.0e-18
 Match length 120
 % identity 42
 NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis

0958-1015-1010

Seq. No.	401138
Seq. ID	LIB3431-040-P1-K2-H8
Method	BLASTX
NCBI GI	g2407281
BLAST score	616
E value	3.0e-64
Match length	118
% identity	97
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

```
Seq. No.          401139
Seq. ID           LIB3431-040-P1-K2-H9
Method            BLASTX
NCBI GI           g2072555
BLAST score       348
E value           7.0e-33
Match length      62
% identity        98
NCBI Description   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
```

Seq. No.	401140
Seq. ID	LIB3431-040-P1-N1-A10
Method	BLASTN
NCBI GI	g2072554
BLAST score	301
E value	1.0e-169
Match length	333
% identity	98
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

```
Seq. No.      401141
Seq. ID       LIB3431-040-P1-N1-B12
Method        BLASTX
NCBI GI       g2754849
BLAST score   169
E value       7.0e-12
Match length  42
% identity    79
NCBI Description (AF039000) putative serine-glyoxylate aminotransferase
               [Fritillaria agrestis]
```


Method	BLASTN
NCBI GI	g4138289
BLAST score	354
E value	0.0e+00
Match length	354
% identity	100
NCBI Description	Oryza sativa mRNA for thioredoxin M
Seq. No.	401166
Seq. ID	LIB3431-040-P1-N1-G8
Method	BLASTX
NCBI GI	g3080420
BLAST score	175
E value	2.0e-12
Match length	43
% identity	74
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]
Seq. No.	401167
Seq. ID	LIB3431-040-P1-N1-H1
Method	BLASTN
NCBI GI	g2072554
BLAST score	370
E value	0.0e+00
Match length	378
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds
Seq. No.	401168
Seq. ID	LIB3431-040-P1-N1-H12
Method	BLASTX
NCBI GI	g4079798
BLAST score	392
E value	6.0e-38
Match length	79
% identity	96
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]
Seq. No.	401169
Seq. ID	LIB3431-040-P1-N1-H3
Method	BLASTX
NCBI GI	g2662310
BLAST score	158
E value	8.0e-21
Match length	56
% identity	90
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]
Seq. No.	401170
Seq. ID	LIB3431-040-P1-N1-H4
Method	BLASTX
NCBI GI	g3126854
BLAST score	343
E value	2.0e-32

Match length 67
 % identity 97
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401171
 Seq. ID LIB3431-040-P1-N1-H7
 Method BLASTX
 NCBI GI g347451
 BLAST score 376
 E value 4.0e-36
 Match length 69
 % identity 99
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 401172
 Seq. ID LIB3431-040-P1-N1-H9
 Method BLASTN
 NCBI GI g218209
 BLAST score 149
 E value 5.0e-78
 Match length 329
 % identity 96
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 401173
 Seq. ID LIB3431-041-P1-N1-A10
 Method BLASTN
 NCBI GI g3126853
 BLAST score 230
 E value 1.0e-126
 Match length 249
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401174
 Seq. ID LIB3431-041-P1-N1-A2
 Method BLASTX
 NCBI GI g115787
 BLAST score 432
 E value 1.0e-42
 Match length 82
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401175
 Seq. ID LIB3431-041-P1-N1-A3
 Method BLASTX
 NCBI GI g4079798

BLAST score 277
 E value 2.0e-24
 Match length 52
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401176
 Seq. ID LIB3431-041-P1-N1-A4
 Method BLASTX
 NCBI GI g2982301
 BLAST score 255
 E value 8.0e-22
 Match length 91
 % identity 55
 NCBI Description (AF051235) YGL010w-like protein [Picea mariana]

Seq. No. 401177
 Seq. ID LIB3431-041-P1-N1-A6
 Method BLASTX
 NCBI GI g6093827
 BLAST score 169
 E value 1.0e-11
 Match length 97
 % identity 41
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_2956690_emb_CAA11248 (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No. 401178
 Seq. ID LIB3431-041-P1-N1-A7
 Method BLASTX
 NCBI GI g120661
 BLAST score 225
 E value 2.0e-18
 Match length 43
 % identity 95
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 401179
 Seq. ID LIB3431-041-P1-N1-A9
 Method BLASTN
 NCBI GI g11640
 BLAST score 45
 E value 4.0e-16
 Match length 137
 % identity 42
 NCBI Description Liverwort Marchantia polymorpha chloroplast genome DNA

Seq. No. 401180
 Seq. ID LIB3431-041-P1-N1-B1
 Method BLASTN
 NCBI GI g2072554

NCBI GI g2570511
 BLAST score 163
 E value 2.0e-26
 Match length 74
 % identity 80
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 401191
 Seq. ID LIB3431-041-P1-N1-C5
 Method BLASTX
 NCBI GI g6015059
 BLAST score 422
 E value 2.0e-41
 Match length 83
 % identity 100
 NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
 (AF030517) translation elongation factor-1 alpha; EF-1
 alpha [Oryza sativa]

Seq. No. 401192
 Seq. ID LIB3431-041-P1-N1-C8
 Method BLASTX
 NCBI GI g730510
 BLAST score 150
 E value 1.0e-09
 Match length 45
 % identity 67
 NCBI Description RAS-RELATED PROTEIN RIC1 >gi_542150_pir_S38740 GTP-binding
 protein - rice >gi_432607_gb_AAB28535_ (S66160) ras-related
 GTP binding protein possessing GTPase activity=ric1 [Oryza
 sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]
 [Oryza sativa]

Seq. No. 401193
 Seq. ID LIB3431-041-P1-N1-D2
 Method BLASTN
 NCBI GI g6006355
 BLAST score 88
 E value 1.0e-41
 Match length 130
 % identity 46
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401194
 Seq. ID LIB3431-041-P1-N1-D3
 Method BLASTX
 NCBI GI g4877984
 BLAST score 262
 E value 1.0e-22
 Match length 53
 % identity 96
 NCBI Description (AF145755) THA4 [Zea mays]

Seq. No. 401195
 Seq. ID LIB3431-041-P1-N1-D7
 Method BLASTN
 NCBI GI g218154

BLAST score 46
 E value 1.0e-16
 Match length 46
 % identity 100
 NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
 clone:Aldp

Seq. No. 401196
 Seq. ID LIB3431-041-P1-N1-E10
 Method BLASTX
 NCBI GI g3582335
 BLAST score 493
 E value 1.0e-49
 Match length 105
 % identity 84
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 401197
 Seq. ID LIB3431-041-P1-N1-E11
 Method BLASTX
 NCBI GI g3738261
 BLAST score 171
 E value 3.0e-12
 Match length 58
 % identity 67
 NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus
 nigra]

Seq. No. 401198
 Seq. ID LIB3431-041-P1-N1-E5
 Method BLASTN
 NCBI GI g416266
 BLAST score 44
 E value 2.0e-15
 Match length 126
 % identity 83
 NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence

Seq. No. 401199
 Seq. ID LIB3431-041-P1-N1-E6
 Method BLASTN
 NCBI GI g3075487
 BLAST score 308
 E value 1.0e-173
 Match length 315
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No. 401200
 Seq. ID LIB3431-041-P1-N1-E7
 Method BLASTN
 NCBI GI g3885887
 BLAST score 465
 E value 0.0e+00
 Match length 465
 % identity 100

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 401211
Seq. ID LIB3431-041-P1-N1-G3
Method BLASTX
NCBI GI g517500
BLAST score 251
E value 1.0e-21
Match length 73
% identity 70

NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
protein [Zea mays] >gi_444338_prf_1906386A photosystem II
OE17 protein [Pisum sativum]

Seq. No. 401212
Seq. ID LIB3431-041-P1-N1-G4
Method BLASTX
NCBI GI g2696804
BLAST score 152
E value 5.0e-10
Match length 28
% identity 100
NCBI Description (AB009665) water channel protein [Oryza sativa]

Seq. No. 401213
Seq. ID LIB3431-041-P1-N1-H3
Method BLASTX
NCBI GI g347451
BLAST score 351
E value 4.0e-33
Match length 69
% identity 96
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
sativa]

Seq. No. 401214
Seq. ID LIB3431-041-P1-N1-H6
Method BLASTN
NCBI GI g2570512
BLAST score 48
E value 2.0e-18
Match length 48
% identity 100
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete
cds

Seq. No. 401215
Seq. ID LIB3431-041-P1-N1-H7
Method BLASTX
NCBI GI g5410350
BLAST score 216
E value 3.0e-17
Match length 45
% identity 91
NCBI Description (AF124045) unknown [Sorghum bicolor]

Seq. No.	401216
Seq. ID	LIB3431-041-P1-N1-H8
Method	BLASTX
NCBI GI	g3126854
BLAST score	235
E value	1.0e-19
Match length	55
% identity	84
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401217
Seq. ID	LIB3431-041-P2-K1-A2
Method	BLASTX
NCBI GI	g320618
BLAST score	380
E value	3.0e-59
Match length	135
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	401218
Seq. ID	LIB3431-041-P2-K1-A3
Method	BLASTX
NCBI GI	g4079798
BLAST score	218
E value	3.0e-18
Match length	50
% identity	90
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]
Seq. No.	401219
Seq. ID	LIB3431-041-P2-K1-A7
Method	BLASTX
NCBI GI	g120657
BLAST score	575
E value	2.0e-59
Match length	136
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66024_pir_DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_(X15408) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.	401220
Seq. ID	LIB3431-041-P2-K1-B1
Method	BLASTN
NCBI GI	g6103440
BLAST score	313

E value	1.0e-176
Match length	332
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds
Seq. No.	401221
Seq. ID	LIB3431-041-P2-K1-B10
Method	BLASTX
NCBI GI	g1835731
BLAST score	297
E value	4.0e-31
Match length	90
% identity	80
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.	401222
Seq. ID	LIB3431-041-P2-K1-B11
Method	BLASTX
NCBI GI	g4958922
BLAST score	219
E value	1.0e-17
Match length	88
% identity	53
NCBI Description	(AB027757) NADPH oxidoreductase homolog [Cicer arietinum]
Seq. No.	401223
Seq. ID	LIB3431-041-P2-K1-B12
Method	BLASTX
NCBI GI	g6094430
BLAST score	200
E value	6.0e-16
Match length	70
% identity	60
NCBI Description	TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi_2511533 (AF008121) alpha-tubulin 2 [Eleusine indica]
Seq. No.	401224
Seq. ID	LIB3431-041-P2-K1-B6
Method	BLASTX
NCBI GI	g2570511
BLAST score	494
E value	5.0e-50
Match length	95
% identity	98
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.	401225
Seq. ID	LIB3431-041-P2-K1-B7
Method	BLASTN
NCBI GI	g20262
BLAST score	296
E value	1.0e-166
Match length	328
% identity	98
NCBI Description	O.sativa light-induced mRNA

Seq. No. 401226
 Seq. ID LIB3431-041-P2-K1-B9
 Method BLASTX
 NCBI GI g1652217
 BLAST score 269
 E value 1.0e-23
 Match length 107
 % identity 54
 NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 401227
 Seq. ID LIB3431-041-P2-K1-C11
 Method BLASTX
 NCBI GI g417260
 BLAST score 322
 E value 1.0e-29
 Match length 80
 % identity 75
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 401228
 Seq. ID LIB3431-041-P2-K1-C12
 Method BLASTX
 NCBI GI g4689380
 BLAST score 402
 E value 2.0e-39
 Match length 78
 % identity 95
 NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein
 [Vigna radiata]

Seq. No. 401229
 Seq. ID LIB3431-041-P2-K1-C2
 Method BLASTX
 NCBI GI g4582455
 BLAST score 185
 E value 9.0e-14
 Match length 99
 % identity 36
 NCBI Description (AC007071) putative receptor protein kinase [Arabidopsis
 thaliana]

Seq. No. 401230
 Seq. ID LIB3431-041-P2-K1-C5
 Method BLASTX
 NCBI GI g2662343
 BLAST score 711
 E value 2.0e-75
 Match length 140
 % identity 99
 NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 401231
 Seq. ID LIB3431-041-P2-K1-C7
 Method BLASTX

Method BLASTX
 NCBI GI g5903095
 BLAST score 159
 E value 2.0e-10
 Match length 49
 % identity 61
 NCBI Description (AC008017) Unknown protein [Arabidopsis thaliana]

Seq. No. 401237
 Seq. ID LIB3431-041-P2-K1-D7
 Method BLASTN
 NCBI GI g218154
 BLAST score 46
 E value 1.0e-16
 Match length 46
 % identity 100
 NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No. 401238
 Seq. ID LIB3431-041-P2-K1-E10
 Method BLASTX
 NCBI GI g3582335
 BLAST score 745
 E value 3.0e-88
 Match length 165
 % identity 95
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 401239
 Seq. ID LIB3431-041-P2-K1-E11
 Method BLASTX
 NCBI GI g129915
 BLAST score 493
 E value 9.0e-50
 Match length 131
 % identity 78
 NCBI Description PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
 >gi_66912_pir_TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
 precursor, chloroplast - wheat >gi_21833_emb_CAA33303
 (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum
 aestivum] >gi_3293043_emb_CAA51931_ (X73528)
 phosphoglycerate kinase [Triticum aestivum]

Seq. No. 401240
 Seq. ID LIB3431-041-P2-K1-E12
 Method BLASTX
 NCBI GI g3128167
 BLAST score 202
 E value 2.0e-15
 Match length 155
 % identity 35
 NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
 >gi_3212874 (AC004005) hypothetical protein [Arabidopsis
 thaliana]

Seq. No. 401241

Seq. ID LIB3431-041-P2-K1-E2
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 3.0e-11
 Match length 36
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 401242
 Seq. ID LIB3431-041-P2-K1-E3
 Method BLASTX
 NCBI GI g3986695
 BLAST score 519
 E value 7.0e-53
 Match length 122
 % identity 86
 NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 401243
 Seq. ID LIB3431-041-P2-K1-E5
 Method BLASTX
 NCBI GI g131388
 BLAST score 188
 E value 4.0e-14
 Match length 87
 % identity 56
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 401244
 Seq. ID LIB3431-041-P2-K1-E6
 Method BLASTX
 NCBI GI g3075488
 BLAST score 426
 E value 2.0e-51
 Match length 126
 % identity 84
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 401245
 Seq. ID LIB3431-041-P2-K1-E7
 Method BLASTN
 NCBI GI g3885887
 BLAST score 355
 E value 0.0e+00
 Match length 363
 % identity 100
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 401246

Seq. ID LIB3431-041-P2-K1-E8
 Method BLASTX
 NCBI GI g3386621
 BLAST score 511
 E value 7.0e-52
 Match length 117
 % identity 85
 NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 401247
 Seq. ID LIB3431-041-P2-K1-E9
 Method BLASTX
 NCBI GI g3980400
 BLAST score 487
 E value 5.0e-49
 Match length 166
 % identity 58
 NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No. 401248
 Seq. ID LIB3431-041-P2-K1-F1
 Method BLASTX
 NCBI GI g3377797
 BLAST score 295
 E value 1.0e-26
 Match length 116
 % identity 53
 NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No. 401249
 Seq. ID LIB3431-041-P2-K1-F11
 Method BLASTN
 NCBI GI g2072554
 BLAST score 307
 E value 1.0e-172
 Match length 319
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401250
 Seq. ID LIB3431-041-P2-K1-F12
 Method BLASTX
 NCBI GI g1835731
 BLAST score 537
 E value 7.0e-55
 Match length 114
 % identity 90
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401251
 Seq. ID LIB3431-041-P2-K1-F2

Method BLASTX
 NCBI GI g131225
 BLAST score 386
 E value 1.0e-37
 Match length 83
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401252
 Seq. ID LIB3431-041-P2-K1-F4
 Method BLASTX
 NCBI GI g2660677
 BLAST score 418
 E value 4.0e-41
 Match length 124
 % identity 62
 NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]

Seq. No. 401253
 Seq. ID LIB3431-041-P2-K1-F5
 Method BLASTN
 NCBI GI g2293567
 BLAST score 165
 E value 6.0e-88
 Match length 197
 % identity 96
 NCBI Description Oryza sativa HvB12D homolog mRNA, complete cds

Seq. No. 401254
 Seq. ID LIB3431-041-P2-K1-F6
 Method BLASTN
 NCBI GI g3821780
 BLAST score 36
 E value 8.0e-11
 Match length 36
 % identity 100
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 401255
 Seq. ID LIB3431-041-P2-K1-F7
 Method BLASTX
 NCBI GI g2980805
 BLAST score 596
 E value 8.0e-62
 Match length 145
 % identity 77
 NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 401256
 Seq. ID LIB3431-041-P2-K1-F8
 Method BLASTX
 NCBI GI g4007792
 BLAST score 316
 E value 6.0e-29

Match length 69
 % identity 93
 NCBI Description Hordeum vulgare partial mRNA; clone cMWG0706

Seq. No. 401262
 Seq. ID LIB3431-041-P2-K1-G9
 Method BLASTX
 NCBI GI g119958
 BLAST score 428
 E value 4.0e-42
 Match length 123
 % identity 70
 NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831)
 ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387)
 Fd III [Zea mays] >gi_444686_prf_1907324C
 ferredoxin:ISOTYPE=III [Zea mays]

Seq. No. 401263
 Seq. ID LIB3431-041-P2-K1-H1
 Method BLASTN
 NCBI GI g2570510
 BLAST score 102
 E value 2.0e-50
 Match length 149
 % identity 92
 NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 401264
 Seq. ID LIB3431-041-P2-K1-H10
 Method BLASTX
 NCBI GI g542200
 BLAST score 143
 E value 7.0e-09
 Match length 55
 % identity 53
 NCBI Description hypothetical protein - garden asparagus
 >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No. 401265
 Seq. ID LIB3431-041-P2-K1-H3
 Method BLASTX
 NCBI GI g132105
 BLAST score 682
 E value 6.0e-72
 Match length 148
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No.	401266
Seq. ID	LIB3431-041-P2-K1-H7
Method	BLASTN
NCBI GI	g5410347
BLAST score	90
E value	6.0e-43
Match length	258
% identity	84
NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.	401267
Seq. ID	LIB3431-041-P2-K1-H8
Method	BLASTX
NCBI GI	g3126854
BLAST score	634
E value	2.0e-66
Match length	122
% identity	98
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401268
Seq. ID	LIB3431-042-P1-K1-A1
Method	BLASTX
NCBI GI	g2407281
BLAST score	662
E value	1.0e-69
Match length	129
% identity	95
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]
Seq. No.	401269
Seq. ID	LIB3431-042-P1-K1-A2
Method	BLASTX
NCBI GI	g4733937
BLAST score	343
E value	3.0e-32
Match length	142
% identity	46
NCBI Description	(AF080245) sesquiterpene synthase [Elaeis oleifera]
Seq. No.	401270
Seq. ID	LIB3431-042-P1-K1-A3
Method	BLASTX
NCBI GI	g3183079
BLAST score	620
E value	1.0e-64
Match length	141
% identity	84
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1375075_dbj_BAA12870.1_(D85763) glyoxysomal malate dehydrogenase [Oryza sativa]
Seq. No.	401271
Seq. ID	LIB3431-042-P1-K1-A4
Method	BLASTX

NCBI GI g1261917
 BLAST score 318
 E value 3.0e-29
 Match length 98
 % identity 59
 NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]

Seq. No. 401272
 Seq. ID LIB3431-042-P1-K1-A5
 Method BLASTX
 NCBI GI g2129608
 BLAST score 594
 E value 1.0e-61
 Match length 138
 % identity 81
 NCBI Description GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577 (L38614) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 401273
 Seq. ID LIB3431-042-P1-K1-A8
 Method BLASTX
 NCBI GI g6056199
 BLAST score 281
 E value 6.0e-25
 Match length 116
 % identity 46
 NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]

Seq. No. 401274
 Seq. ID LIB3431-042-P1-K1-A9
 Method BLASTX
 NCBI GI g347451
 BLAST score 255
 E value 6.0e-22
 Match length 99
 % identity 54
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 401275
 Seq. ID LIB3431-042-P1-K1-B1
 Method BLASTX
 NCBI GI g4972067
 BLAST score 247
 E value 6.0e-21
 Match length 106
 % identity 51
 NCBI Description (AL078467) putative protei [Arabidopsis thaliana]

Seq. No. 401276
 Seq. ID LIB3431-042-P1-K1-B11
 Method BLASTN
 NCBI GI g4959460
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100

NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 401277
Seq. ID LIB3431-042-P1-K1-B12
Method BLASTX
NCBI GI g729135
BLAST score 584
E value 2.0e-60
Match length 144
% identity 76
NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
(S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir_S28612
catechol O-methyltransferase (EC 2.1.1.6) - maize
>gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No. 401278
Seq. ID LIB3431-042-P1-K1-B3
Method BLASTX
NCBI GI g5733882
BLAST score 299
E value 5.0e-27
Match length 136
% identity 52
NCBI Description (AC007932) Similar to gb_Y12465 serine/threonine kinase
from Sorghum bicolor and contains a PF_00069 Eukaryotic
protein kinase domain. [Arabidopsis thaliana]

Seq. No. 401279
Seq. ID LIB3431-042-P1-K1-B4
Method BLASTX
NCBI GI g2065017
BLAST score 290
E value 5.0e-26
Match length 115
% identity 46
NCBI Description (Y09822) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401280
Seq. ID LIB3431-042-P1-K1-B5
Method BLASTX
NCBI GI g871931
BLAST score 416
E value 9.0e-41
Match length 111
% identity 78
NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 401281
Seq. ID LIB3431-042-P1-K1-B6
Method BLASTX
NCBI GI g133936
BLAST score 221
E value 6.0e-18
Match length 70
% identity 67
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir_R3RZ3

Method	BLASTX
NCBI GI	g1483563
BLAST score	676
E value	3.0e-71
Match length	139
% identity	91
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

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Seq. No.      401287
Seq. ID       LIB3431-042-P1-K1-C5
Method        BLASTX
NCBI GI       g132105
BLAST score   546
E value       5.0e-56
Match length  129
% identity    82
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

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Seq. No.      401288
Seq. ID      LIB3431-042-P1-K1-C6
Method       BLASTX
NCBI GI      g3915131
BLAST score   613
E value      7.0e-64
Match length  119
% identity   100
NCBI Description  THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
>gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin
h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza
sativa]
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Seq. No.          401289
Seq. ID           LIB3431-042-P1-K1-C7
Method            BLASTX
NCBI GI           g417260
BLAST score       412
E value           2.0e-40
Match length      126
% identity        66
NCBI Description   LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
                  lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
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Seq. No.      401290
Seq. ID      LIB3431-042-P1-K1-C8
Method       BLASTX
NCBI GI      g4079798
BLAST score   335
```

E value 3.0e-31
 Match length 111
 % identity 62
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401291
 Seq. ID LIB3431-042-P1-K1-C9
 Method BLASTX
 NCBI GI g2911068
 BLAST score 199
 E value 2.0e-15
 Match length 43
 % identity 79
 NCBI Description (AL021960) G10-like protein [Arabidopsis thaliana]

Seq. No. 401292
 Seq. ID LIB3431-042-P1-K1-D12
 Method BLASTX
 NCBI GI g322867
 BLAST score 520
 E value 5.0e-53
 Match length 135
 % identity 75
 NCBI Description translation initiation factor eIF-4F isozyme form subunit p82 - wheat

Seq. No. 401293
 Seq. ID LIB3431-042-P1-K1-D3
 Method BLASTX
 NCBI GI g3914603
 BLAST score 287
 E value 1.0e-25
 Match length 134
 % identity 51
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No. 401294
 Seq. ID LIB3431-042-P1-K1-D4
 Method BLASTX
 NCBI GI g733454
 BLAST score 503
 E value 6.0e-51
 Match length 118
 % identity 81
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 401295
 Seq. ID LIB3431-042-P1-K1-D6
 Method BLASTX
 NCBI GI g3913018
 BLAST score 740
 E value 9.0e-79

Seq. No. 401300
 Seq. ID LIB3431-042-P1-K1-E2
 Method BLASTX
 NCBI GI g100796
 BLAST score 712
 E value 2.0e-75
 Match length 143
 % identity 93
 NCBI Description phosphoribulokinase (EC 2.7.1.19) - wheat

Seq. No. 401301
 Seq. ID LIB3431-042-P1-K1-E3
 Method BLASTN
 NCBI GI g902200
 BLAST score 296
 E value 1.0e-166
 Match length 388
 % identity 49
 NCBI Description Z.mays complete chloroplast genome

Seq. No. 401302
 Seq. ID LIB3431-042-P1-K1-E5
 Method BLASTX
 NCBI GI g320618
 BLAST score 472
 E value 2.0e-47
 Match length 105
 % identity 85
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401303
 Seq. ID LIB3431-042-P1-K1-E6
 Method BLASTX
 NCBI GI g3582335
 BLAST score 728
 E value 2.0e-77
 Match length 141
 % identity 92
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 401304
 Seq. ID LIB3431-042-P1-K1-E7
 Method BLASTN
 NCBI GI g2072724
 BLAST score 384
 E value 0.0e+00
 Match length 403
 % identity 99
 NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog1

Seq. No. 401305
 Seq. ID LIB3431-042-P1-K1-E8

Method BLASTX
 NCBI GI g132105
 BLAST score 657
 E value 5.0e-69
 Match length 140
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401306
 Seq. ID LIB3431-042-P1-K1-E9
 Method BLASTX
 NCBI GI g2570515
 BLAST score 640
 E value 5.0e-67
 Match length 134
 % identity 96
 NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 401307
 Seq. ID LIB3431-042-P1-K1-F1
 Method BLASTX
 NCBI GI g132105
 BLAST score 677
 E value 2.0e-71
 Match length 132
 % identity 95
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401308
 Seq. ID LIB3431-042-P1-K1-F10
 Method BLASTX
 NCBI GI g82080
 BLAST score 432
 E value 1.0e-42
 Match length 122
 % identity 68
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 401309

Seq. ID LIB3431-042-P1-K1-F11
 Method BLASTN
 NCBI GI g2407280
 BLAST score 44
 E value 4.0e-16
 Match length 56
 % identity 95
 NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 401310
 Seq. ID LIB3431-042-P1-K1-F5
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 401311
 Seq. ID LIB3431-042-P1-K1-F6
 Method BLASTX
 NCBI GI g3868756
 BLAST score 699
 E value 5.0e-74
 Match length 136
 % identity 93
 NCBI Description (D86611) catalase [Oryza sativa]

Seq. No. 401312
 Seq. ID LIB3431-042-P1-K1-F7
 Method BLASTX
 NCBI GI g548603
 BLAST score 372
 E value 1.0e-35
 Match length 113
 % identity 69
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 401313
 Seq. ID LIB3431-042-P1-K1-G1
 Method BLASTX
 NCBI GI g1353352
 BLAST score 197
 E value 4.0e-15
 Match length 54
 % identity 72
 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 401314
 Seq. ID LIB3431-042-P1-K1-G10
 Method BLASTX

[illegible]

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Seq. No.      401325
Seq. ID      LIB3431-042-P1-K1-H10
Method       BLASTX
NCBI GI      g3789954
BLAST score   615
E value      4.0e-64
Match length  115
% identity    99
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
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Seq. No.          401327
Seq. ID           LIB3431-042-P1-K1-H2
Method            BLASTX
NCBI GI           g6093778
BLAST score       370
E value           2.0e-35
Match length      103
% identity        75
NCBI Description   PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3)
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3)
                   >gi_2511574_emb_CAA73619.1_(Y13176) multicatalytic
                   endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520)
                   20S proteasome subunit PAB1 [Arabidopsis thaliana]
                   >gi_4966368_gb_AAD34699.1_AC006341.27 (AC006341) Identical
                   to gb_Y13176 Arabidopsis thaliana mRNA for proteasome
                   subunit prc3. ESTs qb H36972, qb T22551 and qb T13800 come

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from this gene

Seq. No. 401328
Seq. ID LIB3431-042-P1-K1-H3
Method BLASTX
NCBI GI g3420052
BLAST score 485
E value 8.0e-51
Match length 137
% identity 77
NCBI Description (AC004680) putative ubiquinone reductase [Arabidopsis thaliana]

Seq. No. 401329
Seq. ID LIB3431-042-P1-K1-H4
Method BLASTX
NCBI GI g3288821
BLAST score 666
E value 4.0e-70
Match length 138
% identity 90
NCBI Description (AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]
>gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 401330
Seq. ID LIB3431-042-P1-K1-H5
Method BLASTX
NCBI GI g82080
BLAST score 455
E value 2.0e-45
Match length 131
% identity 67
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 401331
Seq. ID LIB3431-042-P1-K1-H6
Method BLASTX
NCBI GI g115815
BLAST score 275
E value 1.0e-24
Match length 57
% identity 91
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN M9 PRECURSOR (LHCII TYPE I CAB-M9) (LHCP) >gi_100866_pir_S13098 chlorophyll a/b-binding protein precursor - maize
>gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

Seq. No. 401332
Seq. ID LIB3431-042-P1-K1-H7
Method BLASTX
NCBI GI g3914466
BLAST score 366

E value 5.0e-35
 Match length 67
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
 (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
 subunit precursor [Zea mays]

Seq. No. 401333
 Seq. ID LIB3431-042-P1-K1-H9
 Method BLASTN
 NCBI GI g3885887
 BLAST score 371
 E value 0.0e+00
 Match length 378
 % identity 100
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
 complete cds

Seq. No. 401334
 Seq. ID LIB3431-042-P1-N1-A3
 Method BLASTX
 NCBI GI g3183079
 BLAST score 210
 E value 1.0e-16
 Match length 58
 % identity 74
 NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
 >gi_1375075_dbj_BAA12870.1 (D85763) glyoxysomal malate
 dehydrogenase [Oryza sativa]

Seq. No. 401335
 Seq. ID LIB3431-042-P1-N1-A4
 Method BLASTX
 NCBI GI g1071925
 BLAST score 194
 E value 9.0e-15
 Match length 51
 % identity 65
 NCBI Description Cw-19 peptide, non specific lipid transfer protein,
 precursor - barley >gi_510528_emb_CAA48623 (X68656) Cw-19
 peptide, non specific lipid transfer protein [Hordeum
 vulgare]

Seq. No. 401336
 Seq. ID LIB3431-042-P1-N1-A5
 Method BLASTX
 NCBI GI g2129825
 BLAST score 391
 E value 1.0e-37
 Match length 93
 % identity 83
 NCBI Description dynamin-like protein phragmoplastin 12 - soybean
 >gi_1217994 (U25547) SDL [Glycine max]

Seq. No. 401337
 Seq. ID LIB3431-042-P1-N1-A8
 Method BLASTX

Match length 44
 % identity 75
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 401343
 Seq. ID LIB3431-042-P1-N1-B6
 Method BLASTN
 NCBI GI g11957
 BLAST score 368
 E value 0.0e+00
 Match length 492
 % identity 95
 NCBI Description Rice complete chloroplast genome

Seq. No. 401344
 Seq. ID LIB3431-042-P1-N1-B8
 Method BLASTX
 NCBI GI g517500
 BLAST score 393
 E value 4.0e-38
 Match length 94
 % identity 82
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 401345
 Seq. ID LIB3431-042-P1-N1-B9
 Method BLASTX
 NCBI GI g517500
 BLAST score 421
 E value 2.0e-41
 Match length 112
 % identity 76
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 401346
 Seq. ID LIB3431-042-P1-N1-C1
 Method BLASTX
 NCBI GI g131225
 BLAST score 311
 E value 1.0e-28
 Match length 76
 % identity 76
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401347
 Seq. ID LIB3431-042-P1-N1-C10
 Method BLASTX
 NCBI GI g2754849
 BLAST score 394
 E value 4.0e-38

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Match length      87
% identity        86
NCBI Description  (AF039000) putative serine-glyoxylate aminotransferase
                  [Fritillaria agrestis]

```

```
Seq. No.          401348
Seq. ID           LIB3431-042-P1-N1-C11
Method            BLASTX
NCBI GI           g132105
BLAST score       421
E value           3.0e-41
Match length      76
% identity         100
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

Seq. No.	401349
Seq. ID	LIB3431-042-P1-N1-C4
Method	BLASTX
NCBI GI	g1483563
BLAST score	265
E value	6.0e-23
Match length	53
% identity	92
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

```
Seq. No.          401350
Seq. ID           LIB3431-042-P1-N1-C5
Method            BLASTX
NCBI GI           g671740
BLAST score       227
E value           1.0e-18
Match length      56
% identity         79
NCBI Description   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
```

```
Seq. No.      401351
Seq. ID      LIB3431-042-P1-N1-C6
Method       BLASTN
NCBI GI      g454881
BLAST score   207
E value      1.0e-113
Match length  234
% identity    97
NCBI Description  Rice gene for thioredoxin h, complete cds
```

```
Seq. No.      401352
Seq. ID      LIB3431-042-P1-N1-C7
Method       BLASTX
```

NCBI GI g417260
 BLAST score 406
 E value 2.0e-39
 Match length 128
 % identity 65
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 401353
 Seq. ID LIB3431-042-P1-N1-C9
 Method BLASTN
 NCBI GI g4079797
 BLAST score 66
 E value 1.0e-28
 Match length 246
 % identity 81
 NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
 complete cds

Seq. No. 401354
 Seq. ID LIB3431-042-P1-N1-D10
 Method BLASTX
 NCBI GI g132105
 BLAST score 522
 E value 4.0e-53
 Match length 94
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401355
 Seq. ID LIB3431-042-P1-N1-D11
 Method BLASTX
 NCBI GI g115787
 BLAST score 402
 E value 5.0e-39
 Match length 77
 % identity 99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401356
 Seq. ID LIB3431-042-P1-N1-D12
 Method BLASTN
 NCBI GI g452439
 BLAST score 68

E value 1.0e-17
 Match length 95
 % identity 47
 NCBI Description (AC009918) unknown protein [Arabidopsis thaliana]

Seq. No. 401362
 Seq. ID LIB3431-042-P1-N1-E2
 Method BLASTX
 NCBI GI g21839
 BLAST score 361
 E value 3.0e-34
 Match length 74
 % identity 96
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 401363
 Seq. ID LIB3431-042-P1-N1-E3
 Method BLASTX
 NCBI GI g1173275
 BLAST score 653
 E value 2.0e-68
 Match length 147
 % identity 91
 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
 >gi_2119068_pir_S58630 ribosomal protein S7 - maize
 chloroplast >gi_902274_emb_CAA60339 (X86563) ribosomal
 protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
 ribosomal protein S7 [Zea mays]

Seq. No. 401364
 Seq. ID LIB3431-042-P1-N1-E5
 Method BLASTX
 NCBI GI g115787
 BLAST score 578
 E value 1.0e-59
 Match length 111
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401365
 Seq. ID LIB3431-042-P1-N1-E6
 Method BLASTX
 NCBI GI g3582335
 BLAST score 191
 E value 2.0e-14
 Match length 62
 % identity 60
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 401366
 Seq. ID LIB3431-042-P1-N1-E7
 Method BLASTN
 NCBI GI g2072726

BLAST score 396
 E value 0.0e+00
 Match length 455
 % identity 97
 NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 401367
 Seq. ID LIB3431-042-P1-N1-E8
 Method BLASTX
 NCBI GI g671740
 BLAST score 320
 E value 1.0e-29
 Match length 61
 % identity 98
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401368
 Seq. ID LIB3431-042-P1-N1-E9
 Method BLASTX
 NCBI GI g132105
 BLAST score 326
 E value 3.0e-30
 Match length 61
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401369
 Seq. ID LIB3431-042-P1-N1-F1
 Method BLASTX
 NCBI GI g671740
 BLAST score 233
 E value 3.0e-19
 Match length 47
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401370
 Seq. ID LIB3431-042-P1-N1-F10
 Method BLASTX
 NCBI GI g115813
 BLAST score 233
 E value 2.0e-19
 Match length 53
 % identity 85
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 401376
Seq. ID LIB3431-042-P1-N1-G1
Method BLASTX
NCBI GI g1353352
BLAST score 197
E value 4.0e-15
Match length 54
% identity 72
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 401377
Seq. ID LIB3431-042-P1-N1-G10
Method BLASTX
NCBI GI g3789954
BLAST score 174
E value 2.0e-12
Match length 31
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 401378
Seq. ID LIB3431-042-P1-N1-G11
Method BLASTN
NCBI GI g4680189
BLAST score 84
E value 3.0e-39
Match length 148
% identity 23
NCBI Description Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No. 401379
Seq. ID LIB3431-042-P1-N1-G2
Method BLASTX
NCBI GI g1708424
BLAST score 274
E value 4.0e-24
Match length 92
% identity 57
NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

Seq. No. 401380
Seq. ID LIB3431-042-P1-N1-G3
Method BLASTN
NCBI GI g1658312
BLAST score 100
E value 9.0e-49
Match length 103
% identity 50
NCBI Description O.sativa osr40g2 gene

Seq. No. 401381
 Seq. ID LIB3431-042-P1-N1-G4
 Method BLASTX
 NCBI GI g132105
 BLAST score 295
 E value 1.0e-26
 Match length 57
 % identity 98
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401382
 Seq. ID LIB3431-042-P1-N1-G6
 Method BLASTX
 NCBI GI g3915088
 BLAST score 254
 E value 9.0e-22
 Match length 75
 % identity 63
 NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi_903872 (L38898) trans-cinnamate 4-monooxygenase [Petroselinum crispum]

Seq. No. 401383
 Seq. ID LIB3431-042-P1-N1-G8
 Method BLASTX
 NCBI GI g1617197
 BLAST score 276
 E value 3.0e-24
 Match length 71
 % identity 70
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401384
 Seq. ID LIB3431-042-P1-N1-G9
 Method BLASTX
 NCBI GI g1617197
 BLAST score 189
 E value 3.0e-14
 Match length 39
 % identity 90
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401385
 Seq. ID LIB3431-042-P1-N1-H1
 Method BLASTX
 NCBI GI g128191
 BLAST score 343

E value 4.0e-32
 Match length 73
 % identity 88
 NCBI Description NITRATE REDUCTASE [NAD(P)H] >gi_66210_pir_RDBHNP nitrate reductase (NAD(P)H) (EC 1.6.6.2) - barley
 >gi_19065_emb_CAA42739_(X60173) nitrate reductase (NAD(P)H) [Hordeum vulgare]

Seq. No. 401386
 Seq. ID LIB3431-042-P1-N1-H10
 Method BLASTN
 NCBI GI g3789953
 BLAST score 68
 E value 3.0e-30
 Match length 100
 % identity 92
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401387
 Seq. ID LIB3431-042-P1-N1-H12
 Method BLASTN
 NCBI GI g5852077
 BLAST score 179
 E value 3.0e-96
 Match length 218
 % identity 96
 NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone: b6015

Seq. No. 401388
 Seq. ID LIB3431-042-P1-N1-H2
 Method BLASTN
 NCBI GI g169820
 BLAST score 90
 E value 7.0e-43
 Match length 373
 % identity 82
 NCBI Description Oryza sativa triosephosphate isomerase (Rictpi) mRNA, complete cds

Seq. No. 401389
 Seq. ID LIB3431-042-P1-N1-H3
 Method BLASTX
 NCBI GI g5734585
 BLAST score 307
 E value 5.0e-28
 Match length 82
 % identity 73
 NCBI Description (AJ245861) putative internal rotenone-insensitive NADH dehydrogenase [Solanum tuberosum]

Seq. No. 401390
 Seq. ID LIB3431-042-P1-N1-H7
 Method BLASTX
 NCBI GI g3914466

BLAST score 366
 E value 5.0e-35
 Match length 67
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
 (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
 subunit precursor [Zea mays]

Seq. No. 401391
 Seq. ID LIB3431-043-P1-K1-A1
 Method BLASTX
 NCBI GI g132105
 BLAST score 735
 E value 4.0e-78
 Match length 156
 % identity 90
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401392
 Seq. ID LIB3431-043-P1-K1-A11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 628
 E value 1.0e-65
 Match length 119
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401393
 Seq. ID LIB3431-043-P1-K1-A12
 Method BLASTN
 NCBI GI g3885887
 BLAST score 112
 E value 2.0e-56
 Match length 143
 % identity 96
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
 complete cds

Seq. No. 401394
 Seq. ID LIB3431-043-P1-K1-A2
 Method BLASTX
 NCBI GI g3150410
 BLAST score 277
 E value 2.0e-24
 Match length 96
 % identity 60
 NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

Seq. No. 401395
 Seq. ID LIB3431-043-P1-K1-A3
 Method BLASTX
 NCBI GI g3004555
 BLAST score 220
 E value 1.0e-17
 Match length 164
 % identity 12
 NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis thaliana]

Seq. No. 401396
 Seq. ID LIB3431-043-P1-K1-A5
 Method BLASTN
 NCBI GI g4959460
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 401397
 Seq. ID LIB3431-043-P1-K1-A7
 Method BLASTX
 NCBI GI g125606
 BLAST score 184
 E value 2.0e-13
 Match length 59
 % identity 61
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No. 401398
 Seq. ID LIB3431-043-P1-K1-A8
 Method BLASTX
 NCBI GI g3551954
 BLAST score 468
 E value 8.0e-47
 Match length 145
 % identity 57
 NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No. 401399
 Seq. ID LIB3431-043-P1-K1-A9
 Method BLASTX
 NCBI GI g2570499
 BLAST score 191
 E value 1.0e-14
 Match length 38
 % identity 100
 NCBI Description (AF022732) 23kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401400

Seq. ID LIB3431-043-P1-K1-B10
 Method BLASTX
 NCBI GI g132105
 BLAST score 690
 E value 8.0e-73
 Match length 147
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401401
 Seq. ID LIB3431-043-P1-K1-B11
 Method BLASTX
 NCBI GI g2499417
 BLAST score 499
 E value 2.0e-50
 Match length 120
 % identity 78
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir_S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 401402
 Seq. ID LIB3431-043-P1-K1-B2
 Method BLASTX
 NCBI GI g4079798
 BLAST score 537
 E value 7.0e-55
 Match length 104
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401403
 Seq. ID LIB3431-043-P1-K1-B3
 Method BLASTX
 NCBI GI g132105
 BLAST score 584
 E value 2.0e-60
 Match length 110
 % identity 97
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401404
 Seq. ID LIB3431-043-P1-K1-B4
 Method BLASTX
 NCBI GI g3258238
 BLAST score 157
 E value 2.0e-10
 Match length 108
 % identity 30
 NCBI Description (AP000007) 224aa long hypothetical protein [Pyrococcus horikoshii]

Seq. No. 401405
 Seq. ID LIB3431-043-P1-K1-B5
 Method BLASTX
 NCBI GI g2982453
 BLAST score 224
 E value 3.0e-22
 Match length 72
 % identity 78
 NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No. 401406
 Seq. ID LIB3431-043-P1-K1-B6
 Method BLASTX
 NCBI GI g132105
 BLAST score 839
 E value 3.0e-90
 Match length 175
 % identity 91
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401407
 Seq. ID LIB3431-043-P1-K1-B9
 Method BLASTX
 NCBI GI g732174
 BLAST score 531
 E value 3.0e-54
 Match length 144
 % identity 67
 NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE K03H1.2 >gi_3878176_emb_CAA82662.1_ (Z29560) similar to DEAH subfamily RNA helicases, especially yeast pre-mRNA splicing factors 22 and 16; cDNA EST EMBL:D27770 comes from this gene; cDNA EST EMBL:D27769 comes from this gene; cDNA EST EMBL:D36247 comes from thi... >gi_4249768_gb_AAD13795_ (AF120269) sex determination

096401a-101000

Seq. No.	401409
Seq. ID	LIB3431-043-P1-K1-C10
Method	BLASTN
NCBI GI	g21832
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Wheat mRNA for chloroplast phosphoglycerate kinase (EC 2.7.2.3)

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Seq. No.      401411
Seq. ID      LIB3431-043-P1-K1-C2
Method       BLASTX
NCBI GI      g115787
BLAST score   489
E value      2.0e-49
Match length  117
% identity    85
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
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51481

Match length 32
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 401413
 Seq. ID LIB3431-043-P1-K1-C5
 Method BLASTX
 NCBI GI g676884
 BLAST score 289
 E value 9.0e-26
 Match length 77
 % identity 71
 NCBI Description (D29681) The expression is induced by Pi starvation.
 [Nicotiana tabacum] >gi_1094819_prf_2106387C Al-induced
 protein [Nicotiana tabacum]

Seq. No. 401414
 Seq. ID LIB3431-043-P1-K1-C6
 Method BLASTN
 NCBI GI g1661159
 BLAST score 81
 E value 5.0e-38
 Match length 85
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b binding protein (kcd1895)
 mRNA, complete cds

Seq. No. 401415
 Seq. ID LIB3431-043-P1-K1-C7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 507
 E value 2.0e-51
 Match length 123
 % identity 81
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401416
 Seq. ID LIB3431-043-P1-K1-C9
 Method BLASTX
 NCBI GI g4587556
 BLAST score 433
 E value 1.0e-42
 Match length 140
 % identity 61
 NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp
 3-pyrophosphohydrolase from Synechocystis sp genome
 gb_D90911. EST gb_W43807 comes from this gene.
 [Arabidopsis thaliana]

Seq. No. 401417
 Seq. ID LIB3431-043-P1-K1-D1
 Method BLASTX
 NCBI GI g2618686
 BLAST score 402

E value 5.0e-39
 Match length 163
 % identity 48
 NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401418
 Seq. ID LIB3431-043-P1-K1-D10
 Method BLASTN
 NCBI GI g3618309
 BLAST score 157
 E value 3.0e-83
 Match length 173
 % identity 97
 NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707

Seq. No. 401419
 Seq. ID LIB3431-043-P1-K1-D12
 Method BLASTX
 NCBI GI g1718097
 BLAST score 448
 E value 2.0e-44
 Match length 125
 % identity 62
 NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir_A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No. 401420
 Seq. ID LIB3431-043-P1-K1-D2
 Method BLASTX
 NCBI GI g671740
 BLAST score 486
 E value 6.0e-49
 Match length 88
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401421
 Seq. ID LIB3431-043-P1-K1-D3
 Method BLASTX
 NCBI GI g115787
 BLAST score 515
 E value 2.0e-52
 Match length 121
 % identity 86
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401422
 Seq. ID LIB3431-043-P1-K1-D5

Method BLASTX
NCBI GI g417260
BLAST score 407
E value 1.0e-39
Match length 128
% identity 65
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
light-regulated gene [Oryza sativa]

Seq. No. 401423
Seq. ID LIB3431-043-P1-K1-D7
Method BLASTX
NCBI GI g320618
BLAST score 530
E value 4.0e-54
Match length 121
% identity 83
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 401424
Seq. ID LIB3431-043-P1-K1-D8
Method BLASTX
NCBI GI g4583548
BLAST score 723
E value 1.0e-76
Match length 183
% identity 78
NCBI Description (AJ010820) chloroplast FtsY homolog [Arabidopsis thaliana]

Seq. No. 401425
Seq. ID LIB3431-043-P1-K1-D9
Method BLASTX
NCBI GI g1749676
BLAST score 147
E value 3.0e-09
Match length 82
% identity 44
NCBI Description (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
EMBL Accession Number Z72990 [Schizosaccharomyces pombe]

Seq. No. 401426
Seq. ID LIB3431-043-P1-K1-E1
Method BLASTN
NCBI GI g2773153
BLAST score 489
E value 0.0e+00
Match length 496
% identity 100
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
(Asr1) mRNA, complete cds

Seq. No. 401427

Seq. ID LIB3431-043-P1-K1-E10
 Method BLASTX
 NCBI GI g82080
 BLAST score 378
 E value 3.0e-36
 Match length 112
 % identity 66
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 401428
 Seq. ID LIB3431-043-P1-K1-E12
 Method BLASTX
 NCBI GI g115787
 BLAST score 741
 E value 1.0e-78
 Match length 169
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401429
 Seq. ID LIB3431-043-P1-K1-E3
 Method BLASTN
 NCBI GI g6006355
 BLAST score 221
 E value 1.0e-121
 Match length 297
 % identity 100
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401430
 Seq. ID LIB3431-043-P1-K1-E5
 Method BLASTX
 NCBI GI g3256035
 BLAST score 238
 E value 9.0e-20
 Match length 135
 % identity 39
 NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum
 bicolor]

Seq. No. 401431
 Seq. ID LIB3431-043-P1-K1-E6
 Method BLASTX
 NCBI GI g3789954
 BLAST score 465
 E value 2.0e-46
 Match length 87
 % identity 98
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

```

Seq. No.          401432
Seq. ID           LIB3431-043-P1-K1-E8
Method            BLASTX
NCBI GI           g729478
BLAST score       413
E value           2.0e-40
Match length      158
% identity        53
NCBI Description  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                  >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
                  (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
                  a region of the predicted gene.; similar to
                  ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

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Seq. No.	401433
Seq. ID	LIB3431-043-P1-K1-F12
Method	BLASTX
NCBI GI	g4585882
BLAST score	721
E value	2.0e-76
Match length	159
% identity	81
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

```
Seq. No.          401434
Seq. ID           LIB3431-043-P1-K1-F2
Method            BLASTX
NCBI GI           g2407281
BLAST score       688
E value           2.0e-72
Match length      133
% identity         97
NCBI Description   (AF017363) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
```

```
Seq. No.          401435
Seq. ID           LIB3431-043-P1-K1-F6
Method            BLASTX
NCBI GI           g2443402
BLAST score       824
E value           2.0e-88
Match length      162
% identity         100
NCBI Description   (D87745) orthophosphate dikinase [Oryza sativa]
                   >gi_2443405_dbj_BAA22420_ (D87952) orthophosphate dikinase
                   [Oryza sativa]
```

```
Seq. No.          401436
Seq. ID           LIB3431-043-P1-K1-F8
Method            BLASTX
NCBI GI           g2739375
BLAST score       150
E value           2.0e-09
Match length      95
% identity        41
```

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 401437
Seq. ID LIB3431-043-P1-K1-G1
Method BLASTX
NCBI GI g417488
BLAST score 580
E value 3.0e-72
Match length 155
% identity 85
NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_100452_pir_A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum]

Seq. No. 401438
Seq. ID LIB3431-043-P1-K1-G11
Method BLASTX
NCBI GI g3126854
BLAST score 581
E value 3.0e-60
Match length 109
% identity 100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401439
Seq. ID LIB3431-043-P1-K1-G12
Method BLASTX
NCBI GI g131388
BLAST score 469
E value 7.0e-47
Match length 145
% identity 69
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 401440
Seq. ID LIB3431-043-P1-K1-G3
Method BLASTX
NCBI GI g3126854
BLAST score 671
E value 2.0e-76
Match length 144
% identity 99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401441
Seq. ID LIB3431-043-P1-K1-G4
Method BLASTX
NCBI GI g5596468
BLAST score 266
E value 4.0e-23

Match length 82
 % identity 59
 NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

Seq. No. 401442
 Seq. ID LIB3431-043-P1-K1-G5
 Method BLASTX
 NCBI GI g4454459
 BLAST score 564
 E value 5.0e-58
 Match length 133
 % identity 82
 NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 401443
 Seq. ID LIB3431-043-P1-K1-G7
 Method BLASTX
 NCBI GI g5091616
 BLAST score 643
 E value 3.0e-67
 Match length 202
 % identity 65
 NCBI Description (AC007454) F23M19.3 [Arabidopsis thaliana]

Seq. No. 401444
 Seq. ID LIB3431-043-P1-K1-G8
 Method BLASTX
 NCBI GI g115787
 BLAST score 586
 E value 1.0e-60
 Match length 133
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401445
 Seq. ID LIB3431-043-P1-K1-G9
 Method BLASTX
 NCBI GI g115787
 BLAST score 554
 E value 5.0e-57
 Match length 126
 % identity 87
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401446
 Seq. ID LIB3431-043-P1-K1-H1
 Method BLASTX
 NCBI GI g5926718
 BLAST score 544

carboxylase (RuBPC) [Oryza sativa]

Seq. No. 401451
 Seq. ID LIB3431-043-P1-K1-H6
 Method BLASTX
 NCBI GI g3986110
 BLAST score 431
 E value 2.0e-42
 Match length 121
 % identity 69
 NCBI Description (AB012716) heat shock protein 70 cognate [Salix gilgiana]

Seq. No. 401452
 Seq. ID LIB3431-043-P1-K1-H8
 Method BLASTX
 NCBI GI g5669656
 BLAST score 273
 E value 6.0e-24
 Match length 98
 % identity 56
 NCBI Description (AF096263) ER33 protein [Lycopersicon esculentum]

Seq. No. 401453
 Seq. ID LIB3431-043-P1-N1-A11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 300
 E value 3.0e-27
 Match length 57
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401454
 Seq. ID LIB3431-043-P1-N1-A12
 Method BLASTN
 NCBI GI g3885887
 BLAST score 389
 E value 0.0e+00
 Match length 397
 % identity 99
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 401455
 Seq. ID LIB3431-043-P1-N1-A4
 Method BLASTN
 NCBI GI g11957
 BLAST score 98
 E value 1.0e-47
 Match length 340
 % identity 41
 NCBI Description Rice complete chloroplast genome

Seq. No. 401456
 Seq. ID LIB3431-043-P1-N1-A9
 Method BLASTX
 NCBI GI g4079798

BLAST score 339
 E value 9.0e-32
 Match length 66
 % identity 98
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401457
 Seq. ID LIB3431-043-P1-N1-B10
 Method BLASTX
 NCBI GI g132105
 BLAST score 508
 E value 1.0e-51
 Match length 91
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401458
 Seq. ID LIB3431-043-P1-N1-B11
 Method BLASTX
 NCBI GI g2499417
 BLAST score 309
 E value 3.0e-28
 Match length 71
 % identity 82
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir_S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 401459
 Seq. ID LIB3431-043-P1-N1-B2
 Method BLASTX
 NCBI GI g4079798
 BLAST score 183
 E value 2.0e-13
 Match length 34
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401460
 Seq. ID LIB3431-043-P1-N1-B3
 Method BLASTX
 NCBI GI g347451
 BLAST score 248
 E value 4.0e-21
 Match length 48
 % identity 100

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 401461
Seq. ID LIB3431-043-P1-N1-B4
Method BLASTN
NCBI GI g20262
BLAST score 191
E value 1.0e-103
Match length 379
% identity 88
NCBI Description O.sativa light-induced mRNA

Seq. No. 401462
Seq. ID LIB3431-043-P1-N1-B6
Method BLASTX
NCBI GI g132105
BLAST score 165
E value 2.0e-11
Match length 32
% identity 97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401463
Seq. ID LIB3431-043-P1-N1-C1
Method BLASTX
NCBI GI g115787
BLAST score 409
E value 6.0e-40
Match length 77
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401464
Seq. ID LIB3431-043-P1-N1-C12
Method BLASTN
NCBI GI g5360229
BLAST score 397
E value 0.0e+00
Match length 401
% identity 100
NCBI Description Oryza sativa mRNA for Ran, complete cds

Seq. No. 401465
Seq. ID LIB3431-043-P1-N1-C2

Method BLASTX
 NCBI GI g226263
 BLAST score 213
 E value 5.0e-17
 Match length 47
 % identity 85
 NCBI Description chlorophyll a/b binding protein [Glycine max]

Seq. No. 401466
 Seq. ID LIB3431-043-P1-N1-C7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 314
 E value 8.0e-29
 Match length 80
 % identity 79
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401467
 Seq. ID LIB3431-043-P1-N1-D1
 Method BLASTX
 NCBI GI g1661160
 BLAST score 185
 E value 7.0e-14
 Match length 54
 % identity 69
 NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401468
 Seq. ID LIB3431-043-P1-N1-D10
 Method BLASTX
 NCBI GI g3618310
 BLAST score 367
 E value 4.0e-35
 Match length 70
 % identity 100
 NCBI Description (AB001883) zinc finger protein [Oryza sativa]

Seq. No. 401469
 Seq. ID LIB3431-043-P1-N1-D2
 Method BLASTX
 NCBI GI g671740
 BLAST score 383
 E value 5.0e-37
 Match length 71
 % identity 99
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401470
 Seq. ID LIB3431-043-P1-N1-D3
 Method BLASTX
 NCBI GI g4512125
 BLAST score 243
 E value 1.0e-20
 Match length 45
 % identity 100

NCBI Description (AF133340) putative chlorophyll a/b-binding protein
[Phalaenopsis sp. 'KCbutterfly']

Seq. No. 401471
Seq. ID LIB3431-043-P1-N1-D5
Method BLASTX
NCBI GI g417260
BLAST score 300
E value 3.0e-27
Match length 76
% identity 75

NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
light-regulated gene [Oryza sativa]

Seq. No. 401472
Seq. ID LIB3431-043-P1-N1-D7
Method BLASTX
NCBI GI g115787
BLAST score 428
E value 3.0e-42
Match length 81
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109_
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 401473
Seq. ID LIB3431-043-P1-N1-D8
Method BLASTX
NCBI GI g4583548
BLAST score 346
E value 1.0e-32
Match length 79
% identity 85

NCBI Description (AJ010820) chloroplast FtsY homolog [Arabidopsis thaliana]

Seq. No. 401474
Seq. ID LIB3431-043-P1-N1-D9
Method BLASTX
NCBI GI g1749676
BLAST score 143
E value 9.0e-09
Match length 76
% identity 45

NCBI Description (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
EMBL Accession Number Z72990 [Schizosaccharomyces pombe]

Seq. No. 401475
Seq. ID LIB3431-043-P1-N1-E10
Method BLASTX
NCBI GI g115813
BLAST score 253
E value 1.0e-21
Match length 61

% identity 80
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 401476
Seq. ID LIB3431-043-P1-N1-E12
Method BLASTX
NCBI GI g3036946
BLAST score 271
E value 8.0e-24
Match length 52
% identity 98
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 401477
Seq. ID LIB3431-043-P1-N1-E3
Method BLASTN
NCBI GI g6006355
BLAST score 43
E value 7.0e-15
Match length 123
% identity 84
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401478
Seq. ID LIB3431-043-P1-N1-E5
Method BLASTX
NCBI GI g3256035
BLAST score 195
E value 7.0e-15
Match length 67
% identity 55
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No. 401479
Seq. ID LIB3431-043-P1-N1-E7
Method BLASTX
NCBI GI g128690
BLAST score 535
E value 1.0e-54
Match length 118
% identity 89
NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST >gi_66161_pir_DERZN3 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_(X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa] >gi_226610_prf_1603356AG NADH dehydrogenase ND3 [Oryza sativa]

Seq. No. 401480
Seq. ID LIB3431-043-P1-N1-E8
Method BLASTN
NCBI GI g3819688
BLAST score 41

Match length	63
% identity	89
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

```
Seq. No.      401486
Seq. ID      LIB3431-043-P1-N1-G1
Method       BLASTX
NCBI GI      g417488
BLAST score   152
E value      4.0e-16
Match length  51
% identity    81
NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
H) >gi_100452_pir_A40995 starch phosphorylase (EC 2.4.1.1)
H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
type H isozyme [Solanum tuberosum]
```

```
Seq. No.      401487
Seq. ID       LIB3431-043-P1-N1-G10
Method        BLASTX
NCBI GI       g4006895
BLAST score    158
E value        3.0e-10
Match length   51
% identity     49
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      401488
Seq. ID      LIB3431-043-P1-N1-G11
Method       BLASTX
NCBI GI      g3126854
BLAST score   277
E value      2.0e-24
Match length  52
% identity    100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      401489
Seq. ID      LIB3431-043-P1-N1-G3
Method       BLASTX
NCBI GI      g3126854
BLAST score   200
E value      2.0e-19
Match length  53
% identity    98
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

Seq. No.	401490
Seq. ID	LIB3431-043-P1-N1-G4
Method	BLASTX
NCBI GI	g5596468
BLAST score	145
E value	5.0e-09
Match length	43
% identity	65
NCBI Description	(AL096882) putative protein [Arabidopsis thaliana]

```
Seq. No.      401491
Seq. ID      LIB3431-043-P1-N1-G8
Method       BLASTX
NCBI GI      g3036942
BLAST score   247
E value      5.0e-21
Match length  46
% identity    100
NCBI Description (AB012636) light harvesting chlorophyll a/b-binding protein
[Nicotiana glauca]
```

Seq. No.	401492
Seq. ID	LIB3431-043-P1-N1-G9
Method	BLASTN
NCBI GI	g20181
BLAST score	52
E value	3.0e-20
Match length	72
% identity	93
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

```
Seq. No.          401493
Seq. ID           LIB3431-043-P1-N1-H1
Method            BLASTX
NCBI GI           g303736
BLAST score       152
E value           7.0e-10
Match length      80
% identity        49
NCBI Description   (D12541) GTP-binding protein [Pisum sativum]
                  >gi_738934_prf__2001457B GTP-binding protein [Pisum
                  sativum]
```

Seq. No.	401494
Seq. ID	LIB3431-043-P1-N1-H10
Method	BLASTX
NCBI GI	g167097
BLAST score	151
E value	5.0e-17
Match length	52
% identity	88
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	401495
Seq. ID	LIB3431-043-P1-N1-H11
Method	BLASTN
NCBI GI	g3377792
BLAST score	131
E value	2.0e-67
Match length	284
% identity	87
NCBI Description	Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 401496
 Seq. ID LIB3431-043-P1-N1-H3
 Method BLASTX
 NCBI GI g671740
 BLAST score 163
 E value 4.0e-11
 Match length 31
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401497
 Seq. ID LIB3431-043-P1-N1-H4
 Method BLASTX
 NCBI GI g671740
 BLAST score 301
 E value 3.0e-27
 Match length 57
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401498
 Seq. ID LIB3431-043-P1-N1-H5
 Method BLASTN
 NCBI GI g3218542
 BLAST score 36
 E value 1.0e-10
 Match length 119
 % identity 82
 NCBI Description Oryza sativa AOX1b and AOX1a genes, complete cds

Seq. No. 401499
 Seq. ID LIB3431-043-P1-N1-H6
 Method BLASTN
 NCBI GI g473216
 BLAST score 36
 E value 1.0e-10
 Match length 44
 % identity 95
 NCBI Description P.sativum (little marvel) HSC71.0 mRNA

Seq. No. 401500
 Seq. ID LIB3431-044-P1-K1-A1
 Method BLASTX
 NCBI GI g320618
 BLAST score 457
 E value 1.0e-45
 Match length 106
 % identity 83
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401501

Seq. ID LIB3431-044-P1-K1-A6
 Method BLASTX
 NCBI GI g1835731
 BLAST score 594
 E value 2.0e-61
 Match length 126
 % identity 91
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401507
 Seq. ID LIB3431-044-P1-K1-A7
 Method BLASTX
 NCBI GI g729477
 BLAST score 603
 E value 1.0e-62
 Match length 126
 % identity 87
 NCBI Description FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
 >gi_320548_pir_A44974 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - common ice plant >gi_167256 (M25528) ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1) [Mesembryanthemum crystallinum] >gi_226768_prf_1604475A ferredoxin NADP reductase [Mesembryanthemum crystallinum]

Seq. No. 401508
 Seq. ID LIB3431-044-P1-K1-A8
 Method BLASTX
 NCBI GI g3402711
 BLAST score 349
 E value 5.0e-33
 Match length 120
 % identity 57
 NCBI Description (AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No. 401509
 Seq. ID LIB3431-044-P1-K1-A9
 Method BLASTX
 NCBI GI g3789954
 BLAST score 240
 E value 2.0e-20
 Match length 60
 % identity 77
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 401510
 Seq. ID LIB3431-044-P1-K1-B1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 6.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

% identity 95
 NCBI Description (AF052305) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 401516
 Seq. ID LIB3431-044-P1-K1-B6
 Method BLASTN
 NCBI GI g6015437
 BLAST score 35
 E value 6.0e-10
 Match length 35
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 401517
 Seq. ID LIB3431-044-P1-K1-B7
 Method BLASTX
 NCBI GI g2827150
 BLAST score 559
 E value 2.0e-57
 Match length 148
 % identity 76
 NCBI Description (AF029895) acetyl-coenzyme A carboxylase [Triticum aestivum]

Seq. No. 401518
 Seq. ID LIB3431-044-P1-K1-B8
 Method BLASTX
 NCBI GI g2344892
 BLAST score 213
 E value 7.0e-17
 Match length 68
 % identity 69
 NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 401519
 Seq. ID LIB3431-044-P1-K1-C1
 Method BLASTX
 NCBI GI g1495768
 BLAST score 152
 E value 8.0e-10
 Match length 144
 % identity 45
 NCBI Description (Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No. 401520
 Seq. ID LIB3431-044-P1-K1-C10
 Method BLASTX
 NCBI GI g2130082
 BLAST score 442
 E value 1.0e-43
 Match length 169
 % identity 51
 NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza

longistaminata] >gi_1586408_prf_2203451A receptor
kinase-like protein [Oryza sativa]

Seq. No. 401521
Seq. ID LIB3431-044-P1-K1-C2
Method BLASTX
NCBI GI g2688824
BLAST score 181
E value 3.0e-13
Match length 111
% identity 41
NCBI Description (U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No. 401522
Seq. ID LIB3431-044-P1-K1-C3
Method BLASTX
NCBI GI g548603
BLAST score 295
E value 1.0e-26
Match length 56
% identity 98
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
>gi_478404_pir_JQ2247 photosystem I chain D precursor -
barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 401523
Seq. ID LIB3431-044-P1-K1-C9
Method BLASTX
NCBI GI g3789952
BLAST score 651
E value 2.0e-68
Match length 128
% identity 98
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 401524
Seq. ID LIB3431-044-P1-K1-D1
Method BLASTX
NCBI GI g399213
BLAST score 877
E value 1.0e-94
Match length 181
% identity 96
NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
CD4B PRECURSOR >gi_100190_pir_B35905 CD4B protein - tomato
>gi_170435 (M32604) ATP-dependent protease (CD4B)
[Lycopersicon esculentum]

Seq. No. 401525
Seq. ID LIB3431-044-P1-K1-D12
Method BLASTN
NCBI GI g5295936
BLAST score 46
E value 2.0e-16

Match length 93
 % identity 85
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
 complete sequence

Seq. No. 401526
 Seq. ID LIB3431-044-P1-K1-D2
 Method BLASTX
 NCBI GI g2492515
 BLAST score 662
 E value 2.0e-69
 Match length 155
 % identity 86
 NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
 >gi_2129924_pir_S58298 ATPase - pepper (fragment)
 >gi_929013_emb_CAA62084_ (X90472) ATPase [Capsicum annuum]

Seq. No. 401527
 Seq. ID LIB3431-044-P1-K1-D6
 Method BLASTX
 NCBI GI g1652164
 BLAST score 490
 E value 3.0e-49
 Match length 167
 % identity 61
 NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 401528
 Seq. ID LIB3431-044-P1-K1-E10
 Method BLASTX
 NCBI GI g3618310
 BLAST score 439
 E value 3.0e-43
 Match length 132
 % identity 69
 NCBI Description (AB001883) zinc finger protein [Oryza sativa]

Seq. No. 401529
 Seq. ID LIB3431-044-P1-K1-E11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 784
 E value 8.0e-84
 Match length 151
 % identity 97
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401530
 Seq. ID LIB3431-044-P1-K1-E12
 Method BLASTX
 NCBI GI g131225
 BLAST score 670
 E value 2.0e-70
 Match length 151
 % identity 88
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [*Hordeum vulgare*]

Seq. No. 401531
Seq. ID LIB3431-044-P1-K1-E5
Method BLASTX
NCBI GI g115787
BLAST score 762
E value 3.0e-81
Match length 149
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [*Oryza sativa*]

Seq. No. 401532
Seq. ID LIB3431-044-P1-K1-E6
Method BLASTX
NCBI GI g5042409
BLAST score 442
E value 1.0e-43
Match length 136
% identity 64
NCBI Description (AC006193) Putative membrane related protein [*Arabidopsis thaliana*]

Seq. No. 401533
Seq. ID LIB3431-044-P1-K1-E7
Method BLASTX
NCBI GI g5702231
BLAST score 190
E value 3.0e-14
Match length 108
% identity 44
NCBI Description (AF145386) hypersensitive reaction associated Ca²⁺-binding protein [*Phaseolus vulgaris*]

Seq. No. 401534
Seq. ID LIB3431-044-P1-K1-E8
Method BLASTX
NCBI GI g548605
BLAST score 590
E value 5.0e-61
Match length 130
% identity 90
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [*Hordeum vulgare*]

Seq. No. 401535
Seq. ID LIB3431-044-P1-K1-E9
Method BLASTN
NCBI GI g3821780

E value 1.0e-81
 Match length 170
 % identity 85
 NCBI Description homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
 homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 401541
 Seq. ID LIB3431-044-P1-K1-F6
 Method BLASTX
 NCBI GI g1644427
 BLAST score 452
 E value 7.0e-45
 Match length 130
 % identity 66
 NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 401542
 Seq. ID LIB3431-044-P1-K1-F7
 Method BLASTX
 NCBI GI g1617197
 BLAST score 301
 E value 3.0e-27
 Match length 76
 % identity 75
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401543
 Seq. ID LIB3431-044-P1-K1-F8
 Method BLASTX
 NCBI GI g2072555
 BLAST score 218
 E value 2.0e-17
 Match length 44
 % identity 93
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 401544
 Seq. ID LIB3431-044-P1-K1-F9
 Method BLASTX
 NCBI GI g1352461
 BLAST score 388
 E value 2.0e-37
 Match length 90
 % identity 83
 NCBI Description IN2-2 PROTEIN

Seq. No. 401545
 Seq. ID LIB3431-044-P1-K1-G1
 Method BLASTX
 NCBI GI g4972067
 BLAST score 287
 E value 2.0e-27
 Match length 166
 % identity 44
 NCBI Description (AL078467) putative protei [Arabidopsis thaliana]

Seq. No. 401546
 Seq. ID LIB3431-044-P1-K1-G10
 Method BLASTX
 NCBI GI g3132476
 BLAST score 579
 E value 9.0e-60
 Match length 167
 % identity 66
 NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]

Seq. No. 401547
 Seq. ID LIB3431-044-P1-K1-G11
 Method BLASTX
 NCBI GI g320618
 BLAST score 616
 E value 4.0e-64
 Match length 134
 % identity 87
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401548
 Seq. ID LIB3431-044-P1-K1-G12
 Method BLASTX
 NCBI GI g4490728
 BLAST score 290
 E value 6.0e-26
 Match length 65
 % identity 75
 NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 401549
 Seq. ID LIB3431-044-P1-K1-G3
 Method BLASTN
 NCBI GI g19094
 BLAST score 48
 E value 4.0e-18
 Match length 64
 % identity 94
 NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No. 401550
 Seq. ID LIB3431-044-P1-K1-G4
 Method BLASTX
 NCBI GI g1684851
 BLAST score 212
 E value 6.0e-17
 Match length 62
 % identity 68
 NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No. 401551
 Seq. ID LIB3431-044-P1-K1-G6

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401561
 Seq. ID LIB3431-044-P1-K1-H9
 Method BLASTX
 NCBI GI g132105
 BLAST score 830
 E value 4.0e-89
 Match length 173
 % identity 91
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401562
 Seq. ID LIB3431-044-P1-N1-A1
 Method BLASTN
 NCBI GI g218171
 BLAST score 58
 E value 2.0e-24
 Match length 84
 % identity 93
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
 a/b binding protein of photosystem II (LHCPII), complete
 cds

Seq. No. 401563
 Seq. ID LIB3431-044-P1-N1-A10
 Method BLASTX
 NCBI GI g2982309
 BLAST score 194
 E value 8.0e-15
 Match length 46
 % identity 78
 NCBI Description (AF051239) probable ubiquitin activating enzyme 2 [Picea
 mariana]

Seq. No. 401564
 Seq. ID LIB3431-044-P1-N1-A11
 Method BLASTN
 NCBI GI g2072554
 BLAST score 240
 E value 1.0e-132
 Match length 248

% identity 99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401565
Seq. ID LIB3431-044-P1-N1-A12
Method BLASTN
NCBI GI g2662340
BLAST score 59
E value 8.0e-25
Match length 91
% identity 91
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 401566
Seq. ID LIB3431-044-P1-N1-A4
Method BLASTX
NCBI GI g1173275
BLAST score 640
E value 7.0e-67
Match length 149
% identity 89
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
>gi_2119068_pir_S58630 ribosomal protein S7 - maize
chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
ribosomal protein S7 [Zea mays]

Seq. No. 401567
Seq. ID LIB3431-044-P1-N1-A5
Method BLASTN
NCBI GI g2570512
BLAST score 88
E value 8.0e-42
Match length 195
% identity 96
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 401568
Seq. ID LIB3431-044-P1-N1-A6
Method BLASTX
NCBI GI g1835731
BLAST score 436
E value 4.0e-43
Match length 94
% identity 89
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401569
Seq. ID LIB3431-044-P1-N1-A7
Method BLASTN
NCBI GI g1835730
BLAST score 51
E value 3.0e-20
Match length 59
% identity 97

NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,
complete cds

Seq. No. 401570
Seq. ID LIB3431-044-P1-N1-A9
Method BLASTN
NCBI GI g3789953
BLAST score 267
E value 1.0e-148
Match length 275
% identity 99
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor
(Cab26) mRNA, nuclear gene encoding chloroplast protein,
complete cds

Seq. No. 401571
Seq. ID LIB3431-044-P1-N1-B1
Method BLASTN
NCBI GI g2072554
BLAST score 113
E value 5.0e-57
Match length 164
% identity 93
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
cds

Seq. No. 401572
Seq. ID LIB3431-044-P1-N1-B11
Method BLASTX
NCBI GI g3126854
BLAST score 410
E value 4.0e-40
Match length 78
% identity 99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401573
Seq. ID LIB3431-044-P1-N1-B12
Method BLASTX
NCBI GI g548605
BLAST score 187
E value 2.0e-14
Match length 38
% identity 95
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[Hordeum vulgare]

Seq. No. 401574
Seq. ID LIB3431-044-P1-N1-B2
Method BLASTN
NCBI GI g19086
BLAST score 56
E value 1.0e-22
Match length 100

% identity 91
 NCBI Description Hordeum vulgare pot. psaE mRNA

Seq. No. 401575
 Seq. ID LIB3431-044-P1-N1-B8
 Method BLASTX
 NCBI GI g2344892
 BLAST score 182
 E value 2.0e-13
 Match length 41
 % identity 80
 NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 401576
 Seq. ID LIB3431-044-P1-N1-C11
 Method BLASTN
 NCBI GI g1777706
 BLAST score 59
 E value 1.0e-24
 Match length 71
 % identity 96
 NCBI Description Zea mays 18S ribosomal RNA gene, partial sequence

Seq. No. 401577
 Seq. ID LIB3431-044-P1-N1-C4
 Method BLASTX
 NCBI GI g2829916
 BLAST score 297
 E value 7.0e-27
 Match length 72
 % identity 78
 NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 401578
 Seq. ID LIB3431-044-P1-N1-C9
 Method BLASTN
 NCBI GI g3789951
 BLAST score 157
 E value 6.0e-83
 Match length 300
 % identity 93
 NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401579
 Seq. ID LIB3431-044-P1-N1-D6
 Method BLASTX
 NCBI GI g1652164
 BLAST score 145
 E value 6.0e-09
 Match length 59
 % identity 51
 NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 401580
 Seq. ID LIB3431-044-P1-N1-E10

Seq. No. 401585
 Seq. ID LIB3431-044-P1-N1-F3
 Method BLASTN
 NCBI GI g20181
 BLAST score 76
 E value 1.0e-34
 Match length 118
 % identity 94
 NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 401586
 Seq. ID LIB3431-044-P1-N1-F6
 Method BLASTX
 NCBI GI g1644427
 BLAST score 343
 E value 3.0e-32
 Match length 79
 % identity 80
 NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 401587
 Seq. ID LIB3431-044-P1-N1-F7
 Method BLASTX
 NCBI GI g1617197
 BLAST score 148
 E value 2.0e-09
 Match length 30
 % identity 87
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401588
 Seq. ID LIB3431-044-P1-N1-F8
 Method BLASTN
 NCBI GI g2072554
 BLAST score 209
 E value 1.0e-114
 Match length 265
 % identity 97
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 401589
 Seq. ID LIB3431-044-P1-N1-F9
 Method BLASTX
 NCBI GI g2462750
 BLAST score 204
 E value 6.0e-16
 Match length 58
 % identity 67
 NCBI Description (AC002292) Highly similar to auxin-induced protein
 (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 401590
 Seq. ID LIB3431-044-P1-N1-G11
 Method BLASTX
 NCBI GI g115787

BLAST score 389
 E value 1.0e-37
 Match length 75
 % identity 99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401591
 Seq. ID LIB3431-044-P1-N1-G6
 Method BLASTX
 NCBI GI g1052960
 BLAST score 224
 E value 3.0e-18
 Match length 54
 % identity 81
 NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 401592
 Seq. ID LIB3431-044-P1-N1-G9
 Method BLASTX
 NCBI GI g2072555
 BLAST score 307
 E value 5.0e-28
 Match length 55
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401593
 Seq. ID LIB3431-044-P1-N1-H12
 Method BLASTX
 NCBI GI g4996602
 BLAST score 268
 E value 2.0e-23
 Match length 71
 % identity 75
 NCBI Description (AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana tabacum]

Seq. No. 401594
 Seq. ID LIB3431-044-P1-N1-H2
 Method BLASTN
 NCBI GI g2072726
 BLAST score 430
 E value 0.0e+00
 Match length 468
 % identity 98
 NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 401595
 Seq. ID LIB3431-044-P1-N1-H3
 Method BLASTN
 NCBI GI g2570514

indica]

Seq. No. 401600
Seq. ID LIB3431-045-P1-K1-A10
Method BLASTN
NCBI GI g5441876
BLAST score 106
E value 2.0e-52
Match length 327
% identity 35
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
(contig b)

Seq. No. 401601
Seq. ID LIB3431-045-P1-K1-A12
Method BLASTX
NCBI GI g4689380
BLAST score 640
E value 5.0e-67
Match length 139
% identity 83
NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein
[Vigna radiata]

Seq. No. 401602
Seq. ID LIB3431-045-P1-K1-A3
Method BLASTX
NCBI GI g132105
BLAST score 752
E value 4.0e-80
Match length 160
% identity 90
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 401603
Seq. ID LIB3431-045-P1-K1-A4
Method BLASTX
NCBI GI g132105
BLAST score 794
E value 5.0e-85
Match length 168
% identity 90
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 401604
Seq. ID LIB3431-045-P1-K1-A5
Method BLASTX
NCBI GI g4581146
BLAST score 587
E value 7.0e-61
Match length 142
% identity 82
NCBI Description (AC006919) putative fructose-bisphosphate aldolase,
cytoplasmic [Arabidopsis thaliana]

Seq. No. 401605
Seq. ID LIB3431-045-P1-K1-A6
Method BLASTX
NCBI GI g2407281
BLAST score 814
E value 2.0e-87
Match length 154
% identity 99
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]

Seq. No. 401606
Seq. ID LIB3431-045-P1-K1-A7
Method BLASTX
NCBI GI g871931
BLAST score 517
E value 2.0e-52
Match length 131
% identity 80
NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 401607
Seq. ID LIB3431-045-P1-K1-A8
Method BLASTX
NCBI GI g115787
BLAST score 654
E value 1.0e-68
Match length 127
% identity 98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 401608
Seq. ID LIB3431-045-P1-K1-B1
Method BLASTX
NCBI GI g3885886
BLAST score 502
E value 8.0e-51
Match length 120
% identity 80

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	401609
Seq. ID	LIB3431-045-P1-K1-B10
Method	BLASTX
NCBI GI	g3549656
BLAST score	258
E value	3.0e-22
Match length	91
% identity	58
NCBI Description	(AL031394) putative p

% identity 81
 NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]
 Seq. No. 401614
 Seq. ID LIB3431-045-P1-K1-B6
 Method BLASTX
 NCBI GI g2191152
 BLAST score 222
 E value 8.0e-18
 Match length 117
 % identity 50
 NCBI Description (AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No. 401615
 Seq. ID LIB3431-045-P1-K1-B7
 Method BLASTX
 NCBI GI g1495768
 BLAST score 329
 E value 2.0e-30
 Match length 149
 % identity 46
 NCBI Description (Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No. 401616
 Seq. ID LIB3431-045-P1-K1-B8
 Method BLASTX
 NCBI GI g132105
 BLAST score 690
 E value 8.0e-73
 Match length 147
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401617
 Seq. ID LIB3431-045-P1-K1-B9
 Method BLASTX
 NCBI GI g3169012
 BLAST score 485
 E value 1.0e-48
 Match length 123
 % identity 76
 NCBI Description (AJ002610) putative calmodulin binding transporter protein [Hordeum vulgare]

Seq. No. 401618
 Seq. ID LIB3431-045-P1-K1-C1
 Method BLASTX

NCBI GI g320618
 BLAST score 356
 E value 8.0e-34
 Match length 84
 % identity 81
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401619
 Seq. ID LIB3431-045-P1-K1-C10
 Method BLASTX
 NCBI GI g3885894
 BLAST score 551
 E value 1.0e-56
 Match length 136
 % identity 80
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 401620
 Seq. ID LIB3431-045-P1-K1-C2
 Method BLASTX
 NCBI GI g444790
 BLAST score 255
 E value 7.0e-22
 Match length 124
 % identity 52
 NCBI Description nucleotide translocator [Arabidopsis thaliana]

Seq. No. 401621
 Seq. ID LIB3431-045-P1-K1-C9
 Method BLASTN
 NCBI GI g2306980
 BLAST score 37
 E value 7.0e-12
 Match length 41
 % identity 98
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,
 complete cds

Seq. No. 401622
 Seq. ID LIB3431-045-P1-K1-D11
 Method BLASTX
 NCBI GI g2497903
 BLAST score 220
 E value 9.0e-18
 Match length 59
 % identity 68
 NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2
 >gi_1752831_dbj_BAA14038.1 (D89931) metallothionein-like
 protein [Oryza sativa] >gi_1815628 (U43530)
 metallothionein-like type 2 [Oryza sativa]

Seq. No. 401623
 Seq. ID LIB3431-045-P1-K1-D12

Method BLASTX
 NCBI GI g1174780
 BLAST score 534
 E value 1.0e-54
 Match length 113
 % identity 88
 NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP 2) >gi_320135_pir_PQ0450 tryptophan synthase (EC 4.2.1.20) beta-2 chain precursor - maize (fragment) >gi_168574 (M76685) tryptophan synthase beta-subunit [Zea mays]

Seq. No. 401624
 Seq. ID LIB3431-045-P1-K1-D3
 Method BLASTX
 NCBI GI g5051771
 BLAST score 293
 E value 3.0e-26
 Match length 96
 % identity 66
 NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 401625
 Seq. ID LIB3431-045-P1-K1-D5
 Method BLASTX
 NCBI GI g132105
 BLAST score 511
 E value 6.0e-52
 Match length 115
 % identity 85
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401626
 Seq. ID LIB3431-045-P1-K1-D6
 Method BLASTX
 NCBI GI g2072555
 BLAST score 175
 E value 2.0e-12
 Match length 32
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401627
 Seq. ID LIB3431-045-P1-K1-D8
 Method BLASTX
 NCBI GI g115787
 BLAST score 717
 E value 4.0e-76

Match length 145
 % identity 96
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401628
 Seq. ID LIB3431-045-P1-K1-D9
 Method BLASTX
 NCBI GI g5803254
 BLAST score 223
 E value 4.0e-18
 Match length 104
 % identity 49
 NCBI Description (AP000399) ESTs C97429(C60159), D22427(C11106), AU078031(E31854), D15683(C1084) correspond to a region of the predicted gene; hypothetical protein [Oryza sativa]

Seq. No. 401629
 Seq. ID LIB3431-045-P1-K1-E1
 Method BLASTX
 NCBI GI g1651828
 BLAST score 222
 E value 5.0e-18
 Match length 150
 % identity 40
 NCBI Description (D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]

Seq. No. 401630
 Seq. ID LIB3431-045-P1-K1-E11
 Method BLASTX
 NCBI GI g2244749
 BLAST score 724
 E value 8.0e-77
 Match length 161
 % identity 82
 NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 401631
 Seq. ID LIB3431-045-P1-K1-E2
 Method BLASTX
 NCBI GI g21839
 BLAST score 319
 E value 2.0e-29
 Match length 139
 % identity 59
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 401632
 Seq. ID LIB3431-045-P1-K1-E3
 Method BLASTX
 NCBI GI g4741942
 BLAST score 409
 E value 8.0e-40
 Match length 120

Seq. ID	LIB3431-045-P1-K1-F9
Method	BLASTX
NCBI GI	g5734636
BLAST score	385
E value	5.0e-37
Match length	138
% identity	51
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]
Seq. No.	401644
Seq. ID	LIB3431-045-P1-K1-G1
Method	BLASTX
NCBI GI	g2129538
BLAST score	618
E value	2.0e-64
Match length	132
% identity	89
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]
Seq. No.	401645
Seq. ID	LIB3431-045-P1-K1-G12
Method	BLASTX
NCBI GI	g3914603
BLAST score	836
E value	6.0e-90
Match length	161
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	401646
Seq. ID	LIB3431-045-P1-K1-G2
Method	BLASTX
NCBI GI	g3914603
BLAST score	881
E value	4.0e-95
Match length	169
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	401647
Seq. ID	LIB3431-045-P1-K1-G3
Method	BLASTX
NCBI GI	g3928083
BLAST score	522
E value	4.0e-53
Match length	138
% identity	70
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

E value	2.0e-27
Match length	58
% identity	100
NCBI Description	(AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No.	401659
Seq. ID	LIB3431-045-P1-N1-A10
Method	BLASTN
NCBI GI	g5441876
BLAST score	390
E value	0.0e+00
Match length	454
% identity	96
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	401660
Seq. ID	LIB3431-045-P1-N1-A2
Method	BLASTX
NCBI GI	g1070408
BLAST score	174
E value	2.0e-12
Match length	47
% identity	77
NCBI Description	ferredoxin [2Fe-2S] I - rice

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Seq. No.      401661
Seq. ID       LIB3431-045-P1-N1-A3
Method        BLASTX
NCBI GI       g347451
BLAST score    326
E value       3.0e-30
Match length   61
% identity     100
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
sativa]
```

Seq. No.	401662
Seq. ID	LIB3431-045-P1-N1-A4
Method	BLASTX
NCBI GI	g671740
BLAST score	301
E value	2.0e-27
Match length	57
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

```
Seq. No.          401663
Seq. ID           LIB3431-045-P1-N1-A5
Method            BLASTX
NCBI GI           g5419990
BLAST score       204
E value           5.0e-16
Match length      66
% identity        62
```


NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 401669
 Seq. ID LIB3431-045-P1-N1-B12
 Method BLASTX
 NCBI GI g3892058
 BLAST score 267
 E value 3.0e-23
 Match length 82
 % identity 56
 NCBI Description (AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No. 401670
 Seq. ID LIB3431-045-P1-N1-B2
 Method BLASTN
 NCBI GI g2662342
 BLAST score 58
 E value 7.0e-24
 Match length 89
 % identity 95
 NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 401671
 Seq. ID LIB3431-045-P1-N1-B4
 Method BLASTX
 NCBI GI g132105
 BLAST score 302
 E value 2.0e-27
 Match length 58
 % identity 98
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401672
 Seq. ID LIB3431-045-P1-N1-B8
 Method BLASTX
 NCBI GI g671740
 BLAST score 277
 E value 2.0e-24
 Match length 53
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401673
 Seq. ID LIB3431-045-P1-N1-C1
 Method BLASTN
 NCBI GI g2306980
 BLAST score 50

E value 3.0e-19
 Match length 70
 % identity 93
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No. 401674
 Seq. ID LIB3431-045-P1-N1-C10
 Method BLASTX
 NCBI GI g3885894
 BLAST score 213
 E value 5.0e-17
 Match length 66
 % identity 65
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 401675
 Seq. ID LIB3431-045-P1-N1-C12
 Method BLASTN
 NCBI GI g20181
 BLAST score 79
 E value 3.0e-36
 Match length 107
 % identity 93
 NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No. 401676
 Seq. ID LIB3431-045-P1-N1-C9
 Method BLASTN
 NCBI GI g2306980
 BLAST score 87
 E value 4.0e-41
 Match length 175
 % identity 86
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No. 401677
 Seq. ID LIB3431-045-P1-N1-D10
 Method BLASTX
 NCBI GI g1835731
 BLAST score 359
 E value 4.0e-34
 Match length 80
 % identity 88
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401678
 Seq. ID LIB3431-045-P1-N1-D11
 Method BLASTN
 NCBI GI g1815627
 BLAST score 137
 E value 7.0e-71
 Match length 137
 % identity 100
 NCBI Description Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,

Seq. ID LIB3431-045-P1-N1-G2
Method BLASTX
NCBI GI g167097
BLAST score 151
E value 7.0e-15
Match length 47
% identity 91
NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
[Hordeum vulgare]

Seq. No. 401700
Seq. ID LIB3431-045-P1-N1-G6
Method BLASTX
NCBI GI g3914005
BLAST score 328
E value 2.0e-30
Match length 73
% identity 89
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586
(U85494) LON1 protease [Zea mays]

Seq. No. 401701
Seq. ID LIB3431-045-P1-N1-G8
Method BLASTN
NCBI GI g2570514
BLAST score 206
E value 1.0e-112
Match length 326
% identity 91
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 401702
Seq. ID LIB3431-045-P1-N1-H10
Method BLASTN
NCBI GI g3789951
BLAST score 77
E value 2.0e-35
Match length 105
% identity 93
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
(Cab27) mRNA, nuclear gene encoding chloroplast protein,
complete cds

Seq. No. 401703
Seq. ID LIB3431-045-P1-N1-H2
Method BLASTN
NCBI GI g4105602
BLAST score 343
E value 0.0e+00
Match length 371
% identity 98
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds

Seq. No. 401704
Seq. ID LIB3431-045-P1-N1-H3
Method BLASTN
NCBI GI g5912298

BLAST score 45
 E value 5.0e-16
 Match length 59
 % identity 95
 NCBI Description Oryza sativa mRNA for gigantea homologue, partial

Seq. No. 401705
 Seq. ID LIB3431-045-P1-N1-H4
 Method BLASTX
 NCBI GI g1172977
 BLAST score 327
 E value 2.0e-30
 Match length 69
 % identity 87
 NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 401706
 Seq. ID LIB3431-045-P1-N1-H6
 Method BLASTX
 NCBI GI g3036951
 BLAST score 301
 E value 2.0e-27
 Match length 58
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 401707
 Seq. ID LIB3431-046-P1-K1-A1
 Method BLASTX
 NCBI GI g1353352
 BLAST score 483
 E value 1.0e-48
 Match length 149
 % identity 57
 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 401708
 Seq. ID LIB3431-046-P1-K1-A10
 Method BLASTX
 NCBI GI g6006363
 BLAST score 288
 E value 7.0e-26
 Match length 58
 % identity 98
 NCBI Description (AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No. 401709
 Seq. ID LIB3431-046-P1-K1-A11
 Method BLASTX
 NCBI GI g4105561
 BLAST score 684
 E value 3.0e-72

Match length 139
 % identity 97
 NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No. 401710
 Seq. ID LIB3431-046-P1-K1-A12
 Method BLASTX
 NCBI GI g115787
 BLAST score 438
 E value 3.0e-43
 Match length 106
 % identity 85
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401711
 Seq. ID LIB3431-046-P1-K1-A3
 Method BLASTX
 NCBI GI g320618
 BLAST score 465
 E value 1.0e-46
 Match length 108
 % identity 83
 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 401712
 Seq. ID LIB3431-046-P1-K1-A4
 Method BLASTX
 NCBI GI g2288969
 BLAST score 422
 E value 2.0e-41
 Match length 122
 % identity 70
 NCBI Description (Y12862) glutathione transferase [Zea mays]

Seq. No. 401713
 Seq. ID LIB3431-046-P1-K1-A6
 Method BLASTX
 NCBI GI g320618
 BLAST score 712
 E value 2.0e-75
 Match length 159
 % identity 86
 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 401714

Seq. ID LIB3431-046-P1-K1-A7
 Method BLASTX
 NCBI GI g3075488
 BLAST score 545
 E value 5.0e-56
 Match length 107
 % identity 98
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 401715
 Seq. ID LIB3431-046-P1-K1-A8
 Method BLASTX
 NCBI GI g100454
 BLAST score 627
 E value 2.0e-65
 Match length 154
 % identity 77
 NCBI Description photosystem II oxygen-evolving complex protein 1 - potato
 >gi_809113_emb_CAA35601_ (X17578)- 33kDa precursor protein
 of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 401716
 Seq. ID LIB3431-046-P1-K1-B10
 Method BLASTX
 NCBI GI g6093830
 BLAST score 155
 E value 2.0e-10
 Match length 37
 % identity 81
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
 [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
 PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
 putative photosystem II peptide [Spinacia oleracea]

Seq. No. 401717
 Seq. ID LIB3431-046-P1-K1-B11
 Method BLASTX
 NCBI GI g82080
 BLAST score 433
 E value 9.0e-43
 Match length 124
 % identity 67
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 401718
 Seq. ID LIB3431-046-P1-K1-B12
 Method BLASTX
 NCBI GI g3395439
 BLAST score 266
 E value 4.0e-23
 Match length 81
 % identity 62
 NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401719

BLAST score 583
E value 2.0e-60
Match length 109
% identity 98
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401725
Seq. ID LIB3431-046-P1-K1-C4
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401726
Seq. ID LIB3431-046-P1-K1-C6
Method BLASTN
NCBI GI g3377792
BLAST score 76
E value 4.0e-35
Match length 95
% identity 96
NCBI Description Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 401727
Seq. ID LIB3431-046-P1-K1-C7
Method BLASTX
NCBI GI g132105
BLAST score 632
E value 4.0e-66
Match length 137
% identity 88
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401728
Seq. ID LIB3431-046-P1-K1-C8
Method BLASTX
NCBI GI g1617197
BLAST score 293
E value 2.0e-26
Match length 76
% identity 74
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

09684016-101000

Seq. ID LIB3431-046-P1-K1-D6
 Method BLASTX
 NCBI GI g2072555
 BLAST score 175
 E value 1.0e-12
 Match length 32
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 401735
 Seq. ID LIB3431-046-P1-K1-D8
 Method BLASTX
 NCBI GI g1519249
 BLAST score 697
 E value 1.0e-73
 Match length 146
 % identity 95
 NCBI Description (U65956) GF14-b protein [Oryza sativa]

Seq. No. 401736
 Seq. ID LIB3431-046-P1-K1-D9
 Method BLASTX
 NCBI GI g5738522
 BLAST score 180
 E value 2.0e-13
 Match length 50
 % identity 72
 NCBI Description (AL109846) putative pre-mrna splicing factor atp-dependent
 rna helicase [Schizosaccharomyces pombe]

Seq. No. 401737
 Seq. ID LIB3431-046-P1-K1-E1
 Method BLASTX
 NCBI GI g417260
 BLAST score 381
 E value 1.0e-36
 Match length 121
 % identity 64
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 401738
 Seq. ID LIB3431-046-P1-K1-E12
 Method BLASTX
 NCBI GI g115787
 BLAST score 540
 E value 2.0e-55
 Match length 123
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109_
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401739
 Seq. ID LIB3431-046-P1-K1-E2
 Method BLASTX
 NCBI GI g131225
 BLAST score 607
 E value 4.0e-63
 Match length 127
 % identity 92
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401740
 Seq. ID LIB3431-046-P1-K1-E3
 Method BLASTX
 NCBI GI g6063542
 BLAST score 681
 E value 8.0e-72
 Match length 135
 % identity 100
 NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 401741
 Seq. ID LIB3431-046-P1-K1-E5
 Method BLASTX
 NCBI GI g131205
 BLAST score 178
 E value 9.0e-13
 Match length 36
 % identity 100
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I) >gi_72677_pir_A1RZI photosystem I protein psaI - rice chloroplast >gi_11996_emb_CAA33957_ (X15901) ORF36 [Oryza sativa] >gi_226617_prf_1603356AP photosystem I small peptide [Oryza sativa]

Seq. No. 401742
 Seq. ID LIB3431-046-P1-K1-E6
 Method BLASTX
 NCBI GI g4530126
 BLAST score 236
 E value 2.0e-19
 Match length 90
 % identity 51
 NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No. 401743
 Seq. ID LIB3431-046-P1-K1-E7
 Method BLASTX
 NCBI GI g3334333
 BLAST score 422
 E value 1.0e-41

Match length 103
 % identity 76
 NCBI Description SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi_2660798 (AF034832)
 cytosolic copper/zinc superoxide dismutase
 [Mesembryanthemum crystallinum]

Seq. No. 401744
 Seq. ID LIB3431-046-P1-K1-E8
 Method BLASTX
 NCBI GI g3789954
 BLAST score 563
 E value 4.0e-58
 Match length 120
 % identity 88
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 401745
 Seq. ID LIB3431-046-P1-K1-E9
 Method BLASTX
 NCBI GI g4587556
 BLAST score 284
 E value 2.0e-25
 Match length 103
 % identity 53
 NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp
 3-pyrophosphohydrolase from Synechocystis sp genome
 gb_D90911. EST gb_W43807 comes from this gene.
 [Arabidopsis thaliana]

Seq. No. 401746
 Seq. ID LIB3431-046-P1-K1-F1
 Method BLASTX
 NCBI GI g115787
 BLAST score 529
 E value 5.0e-54
 Match length 121
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401747
 Seq. ID LIB3431-046-P1-K1-F11
 Method BLASTX
 NCBI GI g3345477
 BLAST score 707
 E value 7.0e-75
 Match length 151
 % identity 90
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401748
 Seq. ID LIB3431-046-P1-K1-F3
 Method BLASTX

```

NCBI GI             g4415940
BLAST score         249
E value             3.0e-21
Match length        103
% identity           49
NCBI Description     (AC006418) hypothetical protein [Arabidopsis thaliana]

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```
Seq. No.      401749
Seq. ID      LIB3431-046-P1-K1-F4
Method       BLASTX
NCBI GI      g82080
BLAST score   412
E value      3.0e-40
Match length  117
% identity    68
NCBI Description  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf_1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```

```
Seq. No.          401750
Seq. ID           LIB3431-046-P1-K1-F5
Method            BLASTX
NCBI GI           g1835731
BLAST score       507
E value           2.0e-51
Match length      123
% identity        81
NCBI Description   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

Seq. No.	401751
Seq. ID	LIB3431-046-P1-K1-F6
Method	BLASTX
NCBI GI	g4512125
BLAST score	178
E value	6.0e-13
Match length	32
% identity	100
NCBI Description	(AF133340) putative chlorophyll a/b-binding protein [Phalaenopsis sp. 'KCbutterfly']

```
Seq. No.          401752
Seq. ID           LIB3431-046-P1-K1-F8
Method            BLASTX
NCBI GI           g3914603
BLAST score       680
E value           1.0e-71
Match length      131
% identity        99
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
```

Seq. No.	401753
Seq. ID	LIB3431-046-P1-K1-G1
Method	BLASTX
NCBI GI	q3789952

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260 photosystem II. oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 401758
 Seq. ID LIB3431-046-P1-K1-G6
 Method BLASTN
 NCBI GI g6006355
 BLAST score 108
 E value 8.0e-54
 Match length 164
 % identity 100
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401759
 Seq. ID LIB3431-046-P1-K1-G8
 Method BLASTX
 NCBI GI g2499417
 BLAST score 467
 E value 1.0e-46
 Match length 111
 % identity 80
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
 >gi_1085826_pir_S49248 H-protein - Flaveria anomala
 >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 401760
 Seq. ID LIB3431-046-P1-K1-G9
 Method BLASTX
 NCBI GI g4469020
 BLAST score 602
 E value 2.0e-62
 Match length 132
 % identity 86
 NCBI Description (AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 401761
 Seq. ID LIB3431-046-P1-K1-H1
 Method BLASTX
 NCBI GI g115787
 BLAST score 544
 E value 9.0e-56
 Match length 124
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401762

000101"91048960

Seq. ID LIB3431-046-P1-N1-A11
 Method BLASTN
 NCBI GI g4105560
 BLAST score 101
 E value 2.0e-49
 Match length 164
 % identity 90
 NCBI Description Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA, complete cds

Seq. No. 401772
 Seq. ID LIB3431-046-P1-N1-A4
 Method BLASTX
 NCBI GI g2288969
 BLAST score 205
 E value 5.0e-16
 Match length 68
 % identity 54
 NCBI Description (Y12862) glutathione transferase [Zea mays]

Seq. No. 401773
 Seq. ID LIB3431-046-P1-N1-A6
 Method BLASTX
 NCBI GI g115787
 BLAST score 409
 E value 6.0e-40
 Match length 77
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401774
 Seq. ID LIB3431-046-P1-N1-A7
 Method BLASTX
 NCBI GI g2326947
 BLAST score 224
 E value 3.0e-18
 Match length 44
 % identity 98
 NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]

Seq. No. 401775
 Seq. ID LIB3431-046-P1-N1-A8
 Method BLASTX
 NCBI GI g482311
 BLAST score 244
 E value 9.0e-21
 Match length 50
 % identity 96
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]


```
BLAST score      237
E value          9.0e-20
Match length     44
% identity       100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

Seq. No.	401782
Seq. ID	LIB3431-046-P1-N1-C6
Method	BLASTX
NCBI GI	g167097
BLAST score	165
E value	4.0e-24
Match length	70
% identity	83
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

```
Seq. No.      401783
Seq. ID      LIB3431-046-P1-N1-C7
Method       BLASTX
NCBI GI      g671740
BLAST score   299
E value      4.0e-27
Match length  61
% identity    95
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

```
Seq. No.      401784
Seq. ID      LIB3431-046-P1-N1-D11
Method       BLASTX
NCBI GI      g829283
BLAST score   203
E value      6.0e-16
Match length  48
% identity    83
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
```

```
Seq. No.      401785
Seq. ID      LIB3431-046-P1-N1-D12
Method       BLASTX
NCBI GI      g3377841
BLAST score   182
E value      1.0e-13
Match length  47
% identity    74
NCBI Description (AF075598) contains similarity to phosphofructokinases
(Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
```

```
Seq. No.      401786
Seq. ID      LIB3431-046-P1-N1-D2
Method       BLASTN
NCBI GI      g4099149
BLAST score   43
E value      7.0e-15
```


Seq. ID LIB3431-046-P1-N1-E10
 Method BLASTX
 NCBI GI g729478
 BLAST score 344
 E value 2.0e-32
 Match length 72
 % identity 88
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790). ferredoxin-NADP+
 reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
 (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
 a region of the predicted gene.; similar to
 ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 401793
 Seq. ID LIB3431-046-P1-N1-E12
 Method BLASTX
 NCBI GI g226263
 BLAST score 247
 E value 5.0e-21
 Match length 46
 % identity 100
 NCBI Description chlorophyll a/b binding protein [Glycine max]

Seq. No. 401794
 Seq. ID LIB3431-046-P1-N1-E2
 Method BLASTX
 NCBI GI g131225
 BLAST score 310
 E value 2.0e-28
 Match length 90
 % identity 68
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 401795
 Seq. ID LIB3431-046-P1-N1-E3
 Method BLASTX
 NCBI GI g6063542
 BLAST score 512
 E value 4.0e-52
 Match length 96
 % identity 99
 NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of
 the predicted gene.; similar to glyceraldehyde-3-phosphate
 dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 401796
 Seq. ID LIB3431-046-P1-N1-E5
 Method BLASTX
 NCBI GI g11998
 BLAST score 292
 E value 4.0e-35
 Match length 76
 % identity 93

NCBI Description (X15901) ORF85 [Oryza sativa] >gi_226619_prf_1603356AR ORF 85A [Oryza sativa]

Seq. No. 401797
Seq. ID LIB3431-046-P1-N1-E7
Method BLASTX
NCBI GI g3786214
BLAST score 295
E value 1.0e-26
Match length 74
% identity 74

NCBI Description (AJ002604) high pI CuZn-superoxide dismutase [Pinus sylvestris]

Seq. No. 401798
Seq. ID LIB3431-046-P1-N1-F1
Method BLASTX
NCBI GI g115772
BLAST score 309
E value 3.0e-28
Match length 59
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 401799
Seq. ID LIB3431-046-P1-N1-F11
Method BLASTN
NCBI GI g3345476
BLAST score 173
E value 1.0e-92
Match length 248
% identity 92

NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 401800
Seq. ID LIB3431-046-P1-N1-F3
Method BLASTX
NCBI GI g4415940
BLAST score 172
E value 3.0e-12
Match length 51
% identity 59

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401801
Seq. ID LIB3431-046-P1-N1-F4
Method BLASTX
NCBI GI g115813
BLAST score 243
E value 2.0e-20
Match length 55
% identity 85

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

>gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein
[Hordeum vulgare]

Seq. No. 401807
Seq. ID LIB3431-046-P1-N1-G12
Method BLASTN
NCBI GI g430946
BLAST score 41
E value 1.0e-13
Match length 65
% identity 91
NCBI Description Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds

Seq. No. 401808
Seq. ID LIB3431-046-P1-N1-G3
Method BLASTX
NCBI GI g482311
BLAST score 364
E value 8.0e-35
Match length 73
% identity 99
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 401809
Seq. ID LIB3431-046-P1-N1-G6
Method BLASTN
NCBI GI g6006355
BLAST score 162
E value 4.0e-86
Match length 220
% identity 93
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401810
Seq. ID LIB3431-046-P1-N1-G8
Method BLASTX
NCBI GI g2499417
BLAST score 289
E value 6.0e-26
Match length 68
% identity 78
NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
>gi_1085826_pir_S49248 H-protein - Flaveria anomala
>gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 401811
Seq. ID LIB3431-046-P1-N1-G9
Method BLASTN
NCBI GI g4680196
BLAST score 56
E value 2.0e-22
Match length 108
% identity 88

NCBI Description Sorghum bicolor BAC clone 25.M18, complete sequence

Seq. No. 401812
 Seq. ID LIB3431-046-P1-N1-H10
 Method BLASTN
 NCBI GI g606816
 BLAST score 184
 E value 3.0e-99
 Match length 208
 % identity 97
 NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No. 401813
 Seq. ID LIB3431-046-P1-N1-H4
 Method BLASTN
 NCBI GI g1398998
 BLAST score 165
 E value 9.0e-88
 Match length 272
 % identity 97
 NCBI Description Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II, complete cds

Seq. No. 401814
 Seq. ID LIB3431-046-P1-N1-H7
 Method BLASTX
 NCBI GI g1173347
 BLAST score 172
 E value 3.0e-12
 Match length 39
 % identity 92
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 401815
 Seq. ID LIB3431-046-P1-N1-H9
 Method BLASTN
 NCBI GI g2661765
 BLAST score 46
 E value 1.0e-16
 Match length 82
 % identity 89
 NCBI Description Zea mays mRNA for putative porphobilinogen deaminase

Seq. No. 401816
 Seq. ID LIB3431-047-P1-K1-A11
 Method BLASTX
 NCBI GI g482311
 BLAST score 649
 E value 4.0e-68
 Match length 129
 % identity 98

NCBI GI g132105
 BLAST score 444
 E value 4.0e-44
 Match length 104
 % identity 84
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401827
 Seq. ID LIB3431-047-P1-K1-B2
 Method BLASTN
 NCBI GI g1732362
 BLAST score 35
 E value 4.0e-10
 Match length 43
 % identity 95
 NCBI Description Malus domestica pAFD103 mRNA, partial cds

Seq. No. 401828
 Seq. ID LIB3431-047-P1-K1-B3
 Method BLASTX
 NCBI GI g4808833
 BLAST score 311
 E value 7.0e-29
 Match length 63
 % identity 84
 NCBI Description (AF117125) endoplasmic reticulum-type calcium-transporting
 ATPase 4 [Arabidopsis thaliana]

Seq. No. 401829
 Seq. ID LIB3431-047-P1-K1-B4
 Method BLASTN
 NCBI GI g5670155
 BLAST score 42
 E value 2.0e-14
 Match length 87
 % identity 86
 NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete
 sequence

Seq. No. 401830
 Seq. ID LIB3431-047-P1-K1-B5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 641
 E value 4.0e-67
 Match length 121
 % identity 98
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

09684016-101000

Seq. No. 401831
Seq. ID LIB3431-047-P1-K1-B7
Method BLASTX
NCBI GI g671740
BLAST score 354
E value 1.0e-33
Match length 65
% identity 100
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401832
Seq. ID LIB3431-047-P1-K1-B8
Method BLASTX
NCBI GI g5921799
BLAST score 314
E value 4.0e-29
Match length 87
% identity 71
NCBI Description PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT, MITOCHONDRIAL PRECURSOR (ENDOPEPTIDASE CLP)
>gi_3559935_emb_CAA06443_ (AJ005253) ClpP protease [Mus musculus] >gi_4454289_emb_CAA09966_ (AJ012249) ClpP protease [Mus musculus]

Seq. No. 401833
Seq. ID LIB3431-047-P1-K1-B9
Method BLASTN
NCBI GI g3885887
BLAST score 41
E value 3.0e-14
Match length 45
% identity 98
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 401834
Seq. ID LIB3431-047-P1-K1-C10
Method BLASTN
NCBI GI g5714761
BLAST score 54
E value 2.0e-21
Match length 78
% identity 92
NCBI Description Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete cds

Seq. No. 401835
Seq. ID LIB3431-047-P1-K1-C11
Method BLASTX
NCBI GI g3478700
BLAST score 152
E value 4.0e-10
Match length 41
% identity 66

E value	0.0e+00
Match length	369
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

```

Seq. No.          401846
Seq. ID           LIB3431-047-P1-K1-D3
Method            BLASTX
NCBI GI           g132105
BLAST score       532
E value           2.0e-54
Match length      122
% identity        83
NCBI Description  RIBULOSE BISPHTSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

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Seq. No.      401847
Seq. ID       LIB3431-047-P1-K1-D4
Method        BLASTX
NCBI GI       g534982
BLAST score    264
E value       5.0e-37
Match length  126
% identity    56
NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]
```

```
Seq. No.          401848
Seq. ID          LIB3431-047-P1-K1-D7
Method           BLASTX
NCBI GI         g729478
BLAST score      476
E value         7.0e-48
Match length    102
% identity      85
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
>gi_442481 dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649 dbj_BAA85425.1_
(AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
a region of the predicted gene.; similar to
ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
```

Seq. No.	401849
Seq. ID	LIB3431-047-P1-K1-E1
Method	BLASTX
NCBI GI	g115787
BLAST score	349
E value	4.0e-33
Match length	86
% identity	84

Seq. No. 401865
 Seq. ID LIB3431-047-P1-K1-F9
 Method BLASTX
 NCBI GI g115787
 BLAST score 504
 E value 4.0e-51
 Match length 118
 % identity 86
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401866
 Seq. ID LIB3431-047-P1-K1-G11
 Method BLASTX
 NCBI GI g132105
 BLAST score 470
 E value 3.0e-47
 Match length 107
 % identity 85
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401867
 Seq. ID LIB3431-047-P1-K1-G12
 Method BLASTX
 NCBI GI g3345477
 BLAST score 315
 E value 5.0e-29
 Match length 109
 % identity 59
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401868
 Seq. ID LIB3431-047-P1-K1-G2
 Method BLASTX
 NCBI GI g115771
 BLAST score 864
 E value 3.0e-93
 Match length 170
 % identity 95
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 401869

Seq. ID	LIB3431-047-P1-K1-G4
Method	BLASTX
NCBI GI	g4204276
BLAST score	421
E value	1.0e-41
Match length	107
% identity	75
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	401870
Seq. ID	LIB3431-047-P1-K1-G5
Method	BLASTX
NCBI GI	g2570511
BLAST score	506
E value	2.0e-51
Match length	105
% identity	99
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.	401871
Seq. ID	LIB3431-047-P1-K1-G6
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	2.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	401872
Seq. ID	LIB3431-047-P1-K1-G7
Method	BLASTX
NCBI GI	g3126854
BLAST score	478
E value	3.0e-48
Match length	90
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401873
Seq. ID	LIB3431-047-P1-K1-G8
Method	BLASTX
NCBI GI	g3126854
BLAST score	306
E value	7.0e-48
Match length	119
% identity	85
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401874
Seq. ID	LIB3431-047-P1-K1-G9
Method	BLASTX
NCBI GI	g224293
BLAST score	406
E value	1.0e-39
Match length	82
% identity	99

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401890
 Seq. ID LIB3431-047-P1-N1-A9
 Method BLASTN
 NCBI GI g20369
 BLAST score 291
 E value 1.0e-163
 Match length 326
 % identity 98
 NCBI Description Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31)
 >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase

Seq. No. 401891
 Seq. ID LIB3431-047-P1-N1-B1
 Method BLASTN
 NCBI GI g2072554
 BLAST score 386
 E value 0.0e+00
 Match length 408
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401892
 Seq. ID LIB3431-047-P1-N1-B10
 Method BLASTX
 NCBI GI g6103011
 BLAST score 451
 E value 7.0e-45
 Match length 97
 % identity 51
 NCBI Description (X84225) precursor of photosystem II subunit (22KDa) [Nicotiana tabacum]

Seq. No. 401893
 Seq. ID LIB3431-047-P1-N1-B12
 Method BLASTN
 NCBI GI g218207
 BLAST score 181
 E value 3.0e-97
 Match length 217
 % identity 96
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 401894
 Seq. ID LIB3431-047-P1-N1-B3
 Method BLASTN
 NCBI GI g2160711
 BLAST score 320
 E value 1.0e-180
 Match length 356

(D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401910
 Seq. ID LIB3431-047-P1-N1-D4
 Method BLASTX
 NCBI GI g534982
 BLAST score 214
 E value 2.0e-32
 Match length 106
 % identity 58
 NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No. 401911
 Seq. ID LIB3431-047-P1-N1-D6
 Method BLASTX
 NCBI GI g114622
 BLAST score 249
 E value 4.0e-21
 Match length 53
 % identity 92
 NCBI Description ATP SYNTHASE B CHAIN (SUBUNIT I) >gi_67929_pir_LWRZ1
 H⁺-transporting ATP synthase (EC 3.6.1.34) chain I - rice
 chloroplast >gi_669080_emb_CAA33992_ (X15901) ATPase I
 subunit [Oryza sativa] >gi_226695_prf_1603356W ATPase I
 [Oryza sativa]

Seq. No. 401912
 Seq. ID LIB3431-047-P1-N1-D7
 Method BLASTX
 NCBI GI g729478
 BLAST score 398
 E value 1.0e-38
 Match length 81
 % identity 90
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
 reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
 (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
 a region of the predicted gene.; similar to
 ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 401913
 Seq. ID LIB3431-047-P1-N1-D8
 Method BLASTX
 NCBI GI g5911312
 BLAST score 466
 E value 1.0e-46
 Match length 105
 % identity 80
 NCBI Description (AF026167) ankyrin repeat protein EMB506 [Arabidopsis
 thaliana]

Seq. No. 401914

% identity 96
NCBI Description Rice gene for thioredoxin h, complete cds

Seq. No. 401925
Seq. ID LIB3431-047-P1-N1-F4
Method BLASTN
NCBI GI g455510
BLAST score 132
E value 7.0e-68
Match length 136
% identity 99

NCBI Description Rice mRNA for ferritin, partial sequence

Seq. No. 401926
Seq. ID LIB3431-047-P1-N1-F6
Method BLASTX
NCBI GI g4587615
BLAST score 282
E value 5.0e-25
Match length 80
% identity 66
NCBI Description (AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No. 401927
Seq. ID LIB3431-047-P1-N1-F8
Method BLASTX
NCBI GI g3789954
BLAST score 332
E value 6.0e-31
Match length 63
% identity 98
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 401928
Seq. ID LIB3431-047-P1-N1-G11
Method BLASTX
NCBI GI g132105
BLAST score 393
E value 5.0e-38
Match length 73
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401929
Seq. ID LIB3431-047-P1-N1-G12
Method BLASTN

NCBI GI g3345476
 BLAST score 244
 E value 1.0e-135
 Match length 307
 % identity 95
 NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 401930
 Seq. ID LIB3431-047-P1-N1-G2
 Method BLASTN
 NCBI GI g20181
 BLAST score 56
 E value 7.0e-23
 Match length 67
 % identity 96
 NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No. 401931
 Seq. ID LIB3431-047-P1-N1-G4
 Method BLASTX
 NCBI GI g4204276
 BLAST score 226
 E value 2.0e-18
 Match length 73
 % identity 58
 NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 401932
 Seq. ID LIB3431-047-P1-N1-G5
 Method BLASTX
 NCBI GI g4689380
 BLAST score 260
 E value 9.0e-23
 Match length 55
 % identity 91
 NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

Seq. No. 401933
 Seq. ID LIB3431-047-P1-N1-G7
 Method BLASTX
 NCBI GI g115802
 BLAST score 187
 E value 3.0e-14
 Match length 36
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_(X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No. 401934
 Seq. ID LIB3431-047-P1-N1-G9
 Method BLASTX
 NCBI GI g122106

BLAST score 375
 E value 5.0e-36
 Match length 77
 % identity 97
 NCBI Description HISTONE H4 >gi_70771_pir_HSZM4 histone H4 - maize
 >gi_81642_pir_S06904 histone H4 - Arabidopsis thaliana
 >gi_2119028_pir_S60475 histone H4 - garden pea
 >gi_21795_emb_CAA24924_(X00043) histone H4 [Triticum
 aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis
 thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
 thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
 >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503
 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone
 H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_
 (Z79638) histone H4 homologue [Sesbania rostrata]
 >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
 >gi_4580385_gb_AAD24364.1 AC007184_4 (AC007184) histone H4
 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_
 (AB018245) histone H4-like protein [Solanum melongena]
 >gi_225838_prf_1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 401935
 Seq. ID LIB3431-047-P1-N1-H12
 Method BLASTX
 NCBI GI g1419090
 BLAST score 320
 E value 2.0e-29
 Match length 85
 % identity 72
 NCBI Description (X94968) 37kDa chloroplast inner envelope membrane
 polypeptide precursor [Nicotiana tabacum]

Seq. No. 401936
 Seq. ID LIB3431-047-P1-N1-H4
 Method BLASTN
 NCBI GI g4079797
 BLAST score 51
 E value 1.0e-19
 Match length 106
 % identity 87
 NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
 complete cds

Seq. No. 401937
 Seq. ID LIB3431-048-P1-K1-A10
 Method BLASTX
 NCBI GI g132105
 BLAST score 149
 E value 4.0e-10
 Match length 36
 % identity 83
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

0984016-10000

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Seq. No.      401939
Seq. ID      LIB3431-048-P1-K1-B11
Method       BLASTX
NCBI GI      g4324967
BLAST score   195
E value      2.0e-15
Match length  38
% identity   89
NCBI Description (AF114796) ADP-ribosylation factor [Glycine max]
```

Seq. No.	401941
Seq. ID	LIB3431-048-P1-K1-B2
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

51589

09684016 101000

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Seq. No.      401944
Seq. ID      LIB3431-048-P1-K1-B5
Method       BLASTN
NCBI GI      g20369
BLAST score   143
E value      7.0e-75
Match length  158
% identity    97
NCBI Description  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
synthetase (EC 6.3.1.2) (clone lambda-GS31)
>gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
chloroplast localising glutamine synthetase
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Seq. No.          401946
Seq. ID           LIB3431-048-P1-K1-B8
Method            BLASTX
NCBI GI           g115772
BLAST score       174
E value           5.0e-13
Match length      40
% identity        93
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                  CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi_20178_emb_CAA32108
                  (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                  [Oryza sativa]
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51590

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% identity      95
NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No.       401948
Seq. ID        LIB3431-048-P1-K1-C12
Method         BLASTX
NCBI GI        g1917019
BLAST score    252
E value        4.0e-22
Match length   51
% identity     92
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.       401949
Seq. ID        LIB3431-048-P1-K1-C2
Method         BLASTX
NCBI GI        g2583133
BLAST score    230
E value        5.0e-19
Match length   127
% identity     38
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.       401950
Seq. ID        LIB3431-048-P1-K1-C4
Method         BLASTX
NCBI GI        g4678261
BLAST score    330
E value        3.0e-31
Match length   66
% identity     91
NCBI Description (AL049657) putative proteasome regulatory subunit
[Arabidopsis thaliana]

Seq. No.       401951
Seq. ID        LIB3431-048-P1-K1-C6
Method         BLASTN
NCBI GI        g1245938
BLAST score    35
E value        7.0e-11
Match length   35
% identity     100
NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
heart atrium, mRNA, 2998 nt]

Seq. No.       401952
Seq. ID        LIB3431-048-P1-K1-C8
Method         BLASTN
NCBI GI        g20340
BLAST score    42
E value        9.0e-15
Match length   94
% identity     86
NCBI Description Rice rbcS gene for ribulose 1,5-bisphosphate
carboxylase/oxygenase small subunit (EC 4.1.1.39)

Seq. No.       401953

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carboxylase S [Oryza sativa]

Seq. No. 401963
 Seq. ID LIB3431-048-P1-K1-E5
 Method BLASTX
 NCBI GI g4105131
 BLAST score 139
 E value 6.0e-09
 Match length 31
 % identity 94
 NCBI Description (AF043539) ClpC protease [Spinacia oleracea]

Seq. No. 401964
 Seq. ID LIB3431-048-P1-K1-E7
 Method BLASTX
 NCBI GI g5733874
 BLAST score 351
 E value 2.0e-33
 Match length 112
 % identity 56
 NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No. 401965
 Seq. ID LIB3431-048-P1-K1-F10
 Method BLASTX
 NCBI GI g671740
 BLAST score 315
 E value 1.0e-29
 Match length 68
 % identity 87
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401966
 Seq. ID LIB3431-048-P1-K1-F4
 Method BLASTN
 NCBI GI g2306980
 BLAST score 99
 E value 1.0e-48
 Match length 112
 % identity 97
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No. 401967
 Seq. ID LIB3431-048-P1-K1-F6
 Method BLASTN
 NCBI GI g21843
 BLAST score 39
 E value 1.0e-12
 Match length 76
 % identity 88
 NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II

Seq. No. 401968
 Seq. ID LIB3431-048-P1-K1-F7

Method	BLASTX
NCBI GI	g3126854
BLAST score	151
E value	4.0e-10
Match length	33
% identity	91
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401969
Seq. ID	LIB3431-048-P1-K1-G10
Method	BLASTX
NCBI GI	g733454
BLAST score	266
E value	2.0e-23
Match length	74
% identity	73
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]
Seq. No.	401970
Seq. ID	LIB3431-048-P1-K1-G12
Method	BLASTX
NCBI GI	g2501189
BLAST score	444
E value	2.0e-44
Match length	90
% identity	94
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]
Seq. No.	401971
Seq. ID	LIB3431-048-P1-K1-G4
Method	BLASTX
NCBI GI	g671740
BLAST score	416
E value	6.0e-41
Match length	75
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	401972
Seq. ID	LIB3431-048-P1-K1-G9
Method	BLASTN
NCBI GI	g218207
BLAST score	104
E value	9.0e-52
Match length	112
% identity	98
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone POSSS1139
Seq. No.	401973
Seq. ID	LIB3431-048-P1-K1-H1

Seq. ID LIB3431-048-P1-K1-H8
 Method BLASTX
 NCBI GI g2244786
 BLAST score 158
 E value 4.0e-11
 Match length 39
 % identity 69
 NCBI Description (Z97335) ribonucleoprotein like protein [Arabidopsis thaliana]

Seq. No. 401979
 Seq. ID LIB3431-048-P1-N1-A10
 Method BLASTX
 NCBI GI g132105
 BLAST score 385
 E value 4.0e-37
 Match length 72
 % identity 97
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401980
 Seq. ID LIB3431-048-P1-N1-A12
 Method BLASTX
 NCBI GI g115813
 BLAST score 257
 E value 4.0e-22
 Match length 61
 % identity 82
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 401981
 Seq. ID LIB3431-048-P1-N1-A2
 Method BLASTX
 NCBI GI g2499417
 BLAST score 370
 E value 2.0e-35
 Match length 91
 % identity 77
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir_S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 401982
 Seq. ID LIB3431-048-P1-N1-A3
 Method BLASTX
 NCBI GI g115813

BLAST score 257
 E value 3.0e-22
 Match length 61
 % identity 82
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 401983
 Seq. ID LIB3431-048-P1-N1-A4
 Method BLASTX
 NCBI GI g1663724
 BLAST score 357
 E value 9.0e-34
 Match length 105
 % identity 66
 NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 401984
 Seq. ID LIB3431-048-P1-N1-A6
 Method BLASTN
 NCBI GI g2072554
 BLAST score 63
 E value 1.0e-26
 Match length 174
 % identity 85
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401985
 Seq. ID LIB3431-048-P1-N1-A8
 Method BLASTN
 NCBI GI g3789953
 BLAST score 184
 E value 4.0e-99
 Match length 255
 % identity 93
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401986
 Seq. ID LIB3431-048-P1-N1-B11
 Method BLASTX
 NCBI GI g2293566
 BLAST score 166
 E value 2.0e-11
 Match length 30
 % identity 100
 NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 401987
 Seq. ID LIB3431-048-P1-N1-B4
 Method BLASTX
 NCBI GI g481190
 BLAST score 301
 E value 2.0e-27

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Seq. No. 401998
Seq. ID LIB3431-048-P1-N1-D3
Method BLASTX
NCBI GI g3256035
BLAST score 222
E value 5.0e-18
Match length 81
% identity 52
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No. 401999
Seq. ID LIB3431-048-P1-N1-D5
Method BLASTX
NCBI GI g5257277
BLAST score 331
E value 7.0e-31
Match length 68
% identity 99
NCBI Description (AP000364) ESTs C98431(E0144),C71728(E0144) correspond to a region of the predicted gene.; Similar to Medicago sativa S-adenosyl-L-methionine. (U20736) [Oryza sativa]

Seq. No. 402000
Seq. ID LIB3431-048-P1-N1-D8
Method BLASTN
NCBI GI g435648
BLAST score 69
E value 2.0e-30
Match length 105
% identity 91
NCBI Description Rice mRNA for gamma-Tip, complete cds

Seq. No. 402001
Seq. ID LIB3431-048-P1-N1-D9
Method BLASTX
NCBI GI g1651922
BLAST score 175
E value 2.0e-12
Match length 60
% identity 55
NCBI Description (D90901) hypothetical protein [Synechocystis sp.]

Seq. No. 402002
Seq. ID LIB3431-048-P1-N1-E10
Method BLASTN
NCBI GI g19565
BLAST score 35
E value 4.0e-10
Match length 47
% identity 94
NCBI Description M.liliiflora GADPH mRNA for glycolytic
glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 402003
Seq. ID LIB3431-048-P1-N1-E11
Method BLASTX


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Seq. No.      402012
Seq. ID      LIB3431-048-P1-N1-F4
Method       BLASTN
NCBI GI      g2306980
BLAST score   74
E value      1.0e-33
Match length  88
% identity   97
NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,
               complete cds
```

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Seq. No.      402013
Seq. ID      LIB3431-048-P1-N1-F6
Method       BLASTX
NCBI GI      g482311
BLAST score   298
E value      6.0e-27
Match length  69
% identity    90
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
                (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                complex protein 1 [Oryza sativa]
```

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Seq. No.          402014
Seq. ID           LIB3431-048-P1-N1-F7
Method            BLASTN
NCBI GI           g3126853
BLAST score       122
E value           4.0e-62
Match length      188
% identity        96
NCBI Description  Oryza sativa chlorophyll a/b binding protein (RCABP89)
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
```

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Seq. No.      402015
Seq. ID      LIB3431-048-P1-N1-F8
Method       BLASTN
NCBI GI      g430946
BLAST score   37
E value      3.0e-11
Match length  65
% identity   89
NCBI Description Arabidopsis thaliana PSI type III chlorophyll a/b-binding
                  protein (Lhca3*1) mRNA, complete cds
```

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Seq. No.      402016
Seq. ID      LIB3431-048-P1-N1-G1
Method       BLASTX
NCBI GI      g733454
BLAST score   402
E value      4.0e-39
Match length  81
% identity    95
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
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Seq. No.	402031
Seq. ID	LIB3431-049-P1-K1-B3
Method	BLASTN
NCBI GI	g20181
BLAST score	48
E value	2.0e-18
Match length	72
% identity	92
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	402032
Seq. ID	LIB3431-049-P1-K1-B5
Method	BLASTN
NCBI GI	g4079797
BLAST score	144
E value	2.0e-75
Match length	155
% identity	99
NCBI Description	Oryza sativa 23 kDa polypeptide of photosystem II mRNA, complete cds
Seq. No.	402033
Seq. ID	LIB3431-049-P1-K1-B7
Method	BLASTX
NCBI GI	g549063
BLAST score	276
E value	5.0e-37
Match length	82
% identity	99
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]
Seq. No.	402034
Seq. ID	LIB3431-049-P1-K1-C12
Method	BLASTX
NCBI GI	g606817
BLAST score	661
E value	4.0e-81
Match length	155
% identity	99
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]
Seq. No.	402035
Seq. ID	LIB3431-049-P1-K1-C4
Method	BLASTX
NCBI GI	g1805617
BLAST score	163
E value	5.0e-20
Match length	56
% identity	96
NCBI Description	(D49704) OSH44 transcript; homeobox gene [Oryza sativa]
Seq. No.	402036
Seq. ID	LIB3431-049-P1-K1-C5
Method	BLASTN
NCBI GI	g3885885
BLAST score	191
E value	1.0e-103
Match length	226
% identity	97
NCBI Description	Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA, complete cds

Seq. No. 402037
 Seq. ID LIB3431-049-P1-K1-C7
 Method BLASTN
 NCBI GI g218171
 BLAST score 83
 E value 4.0e-39
 Match length 138
 % identity 91
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No. 402038
 Seq. ID LIB3431-049-P1-K1-C8
 Method BLASTX
 NCBI GI g2739360
 BLAST score 152
 E value 6.0e-18
 Match length 102
 % identity 51
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
 >gi_3075385 (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 402039
 Seq. ID LIB3431-049-P1-K1-D1
 Method BLASTN
 NCBI GI g4218534
 BLAST score 45
 E value 2.0e-16
 Match length 45
 % identity 100
 NCBI Description Triticum sp. mRNA for GRAB1 protein

Seq. No. 402040
 Seq. ID LIB3431-049-P1-K1-D10
 Method BLASTX
 NCBI GI g3789954
 BLAST score 367
 E value 4.0e-45
 Match length 100
 % identity 95
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 402041
 Seq. ID LIB3431-049-P1-K1-D12
 Method BLASTX
 NCBI GI g3676294
 BLAST score 151
 E value 5.0e-21
 Match length 66
 % identity 77
 NCBI Description (U96496) mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Seq. No. 402042

Seq. ID LIB3431-049-P1-K1-D4
 Method BLASTX
 NCBI GI g3126854
 BLAST score 345
 E value 6.0e-35
 Match length 78
 % identity 97
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402043
 Seq. ID LIB3431-049-P1-K1-E10
 Method BLASTN
 NCBI GI g3126853
 BLAST score 150
 E value 6.0e-79
 Match length 222
 % identity 93
 NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)
 mRNA, nuclear gene encoding chloroplast protein, complete
 cds

Seq. No. 402044
 Seq. ID LIB3431-049-P1-K1-E11
 Method BLASTN
 NCBI GI g4138289
 BLAST score 68
 E value 4.0e-30
 Match length 72
 % identity 99
 NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 402045
 Seq. ID LIB3431-049-P1-K1-E9
 Method BLASTN
 NCBI GI g3885891
 BLAST score 80
 E value 7.0e-37
 Match length 95
 % identity 97
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
 mRNA, complete cds

Seq. No. 402046
 Seq. ID LIB3431-049-P1-K1-F12
 Method BLASTX
 NCBI GI g3885894
 BLAST score 266
 E value 9.0e-34
 Match length 91
 % identity 86
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 402047
 Seq. ID LIB3431-049-P1-K1-F2
 Method BLASTX
 NCBI GI g2130089
 BLAST score 219

E value	4.0e-18
Match length	49
% identity	90
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]
Seq. No.	402048
Seq. ID	LIB3431-049-P1-K1-F4
Method	BLASTX
NCBI GI	g320618
BLAST score	332
E value	1.0e-33
Match length	95
% identity	75
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	402049
Seq. ID	LIB3431-049-P1-K1-F6
Method	BLASTN
NCBI GI	g409581
BLAST score	38
E value	1.0e-12
Match length	62
% identity	90
NCBI Description	Rice mRNA for serine carboxypeptidase-like protein
Seq. No.	402050
Seq. ID	LIB3431-049-P1-K1-F8
Method	BLASTN
NCBI GI	g218207
BLAST score	107
E value	2.0e-53
Match length	142
% identity	94
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone POSSS1139
Seq. No.	402051
Seq. ID	LIB3431-049-P1-K1-F9
Method	BLASTN
NCBI GI	g218132
BLAST score	137
E value	3.0e-71
Match length	162
% identity	96
NCBI Description	Rice mRNA for Heat shock protein
Seq. No.	402052
Seq. ID	LIB3431-049-P1-K1-G7
Method	BLASTX

Seq. No. 402078
 Seq. ID LIB3431-049-P1-N1-E11
 Method BLASTN
 NCBI GI g4138289
 BLAST score 163
 E value 2.0e-86
 Match length 324
 % identity 87
 NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 402079
 Seq. ID LIB3431-049-P1-N1-E2
 Method BLASTX
 NCBI GI g128690
 BLAST score 529
 E value 8.0e-54
 Match length 116
 % identity 90
 NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
 >gi_66161_pir_DERZN3 NADH dehydrogenase (ubiquinone) (EC
 1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_
 (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
 >gi_226610_prf_1603356AG NADH dehydrogenase ND3 [Oryza
 sativa]

Seq. No. 402080
 Seq. ID LIB3431-049-P1-N1-E9
 Method BLASTX
 NCBI GI g3885892
 BLAST score 200
 E value 1.0e-15
 Match length 49
 % identity 82
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402081
 Seq. ID LIB3431-049-P1-N1-F12
 Method BLASTX
 NCBI GI g3885894
 BLAST score 178
 E value 5.0e-13
 Match length 59
 % identity 68
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 402082
 Seq. ID LIB3431-049-P1-N1-F2
 Method BLASTX
 NCBI GI g2130089
 BLAST score 439
 E value 2.0e-43
 Match length 88
 % identity 90
 NCBI Description 2-oxoglutarate/malate translocator (clone OMT103),
 mitochondrial membrane - proso millet
 >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
 translocator [Panicum miliaceum]

Seq. ID	LIB3431-049-P1-N1-G3
Method	BLASTN
NCBI GI	g3885891
BLAST score	34
E value	5.0e-10
Match length	58
% identity	90
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds
Seq. No.	402089
Seq. ID	LIB3431-049-P1-N1-G6
Method	BLASTX
NCBI GI	g6006283
BLAST score	162
E value	3.0e-11
Match length	41
% identity	71
NCBI Description	(AB015861) photosystem I subunit PSI-L [Arabidopsis thaliana]
Seq. No.	402090
Seq. ID	LIB3431-049-P1-N1-G7
Method	BLASTX
NCBI GI	g551047
BLAST score	243
E value	2.0e-20
Match length	55
% identity	85
NCBI Description	(X79277) type II LHCI [Lolium temulentum]
Seq. No.	402091
Seq. ID	LIB3431-049-P1-N1-G8
Method	BLASTN
NCBI GI	g218207
BLAST score	180
E value	1.0e-96
Match length	279
% identity	90
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139
Seq. No.	402092
Seq. ID	LIB3431-049-P1-N1-H5
Method	BLASTX
NCBI GI	g4262142
BLAST score	145
E value	5.0e-09
Match length	69
% identity	49
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	402093
Seq. ID	LIB3431-049-P1-N1-H6
Method	BLASTX

NCBI GI g671740
 BLAST score 380
 E value 2.0e-36
 Match length 69
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402094
 Seq. ID LIB3431-049-P1-N1-H7
 Method BLASTX
 NCBI GI g21839
 BLAST score 336
 E value 2.0e-31
 Match length 75
 % identity 87
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402095
 Seq. ID LIB3431-050-P1-K1-A10
 Method BLASTN
 NCBI GI g2062705
 BLAST score 35
 E value 5.0e-10
 Match length 35
 % identity 100
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 402096
 Seq. ID LIB3431-050-P1-K1-A11
 Method BLASTX
 NCBI GI g131192
 BLAST score 449
 E value 1.0e-44
 Match length 97
 % identity 87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
 (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937
 photosystem I chain V precursor - barley
 >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide
 PSI-G precursor [Hordeum vulgare]

Seq. No. 402097
 Seq. ID LIB3431-050-P1-K1-A2
 Method BLASTX
 NCBI GI g132105
 BLAST score 339
 E value 4.0e-32
 Match length 79
 % identity 86
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

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% identity 97
NCBI Description Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS1139

Seq. No. 402103
Seq. ID LIB3431-050-P1-K1-B10
Method BLASTN
NCBI GI g20262
BLAST score 268
E value 1.0e-149
Match length 308
% identity 97
NCBI Description O.sativa light-induced mRNA

Seq. No. 402104
Seq. ID LIB3431-050-P1-K1-B2
Method BLASTX
NCBI GI g320618
BLAST score 290
E value 3.0e-26
Match length 70
% identity 79
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 402105
Seq. ID LIB3431-050-P1-K1-B3
Method BLASTX
NCBI GI g3367596
BLAST score 311
E value 6.0e-32
Match length 98
% identity 70
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 402106
Seq. ID LIB3431-050-P1-K1-B7
Method BLASTX
NCBI GI g2924785
BLAST score 165
E value 2.0e-11
Match length 79
% identity 47
NCBI Description (AC002334) similar to disease resistance protein
[Arabidopsis thaliana]

Seq. No. 402107
Seq. ID LIB3431-050-P1-K1-C1
Method BLASTX
NCBI GI g3236242
BLAST score 435
E value 4.0e-43
Match length 106

% identity 80
 NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 402108
 Seq. ID LIB3431-050-P1-K1-C12
 Method BLASTX
 NCBI GI g82080
 BLAST score 364
 E value 8.0e-35
 Match length 103
 % identity 70
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 402109
 Seq. ID LIB3431-050-P1-K1-C2
 Method BLASTX
 NCBI GI g3036953
 BLAST score 273
 E value 5.0e-24
 Match length 51
 % identity 100
 NCBI Description (AB012640) light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]

Seq. No. 402110
 Seq. ID LIB3431-050-P1-K1-C7
 Method BLASTX
 NCBI GI g3808101
 BLAST score 335
 E value 2.0e-33
 Match length 99
 % identity 70
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 402111
 Seq. ID LIB3431-050-P1-K1-C9
 Method BLASTX
 NCBI GI g132105
 BLAST score 480
 E value 2.0e-48
 Match length 112
 % identity 82
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402112
 Seq. ID LIB3431-050-P1-K1-D1

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Method BLASTX
 NCBI GI g3929924
 BLAST score 210
 E value 4.0e-17
 Match length 41
 % identity 100
 NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 402113
 Seq. ID LIB3431-050-P1-K1-D10
 Method BLASTX
 NCBI GI g462195
 BLAST score 281
 E value 5.0e-25
 Match length 69
 % identity 81
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190 (X51910) GOS2 [Oryza sativa]
 >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 402114
 Seq. ID LIB3431-050-P1-K1-D11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 7.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402115
 Seq. ID LIB3431-050-P1-K1-D2
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 8.0e-11
 Match length 36
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402116
 Seq. ID LIB3431-050-P1-K1-D3
 Method BLASTX
 NCBI GI g1370188
 BLAST score 304
 E value 5.0e-28
 Match length 71
 % identity 79
 NCBI Description (Z73943) RAB7D [Lotus japonicus]

Seq. No. 402117
 Seq. ID LIB3431-050-P1-K1-D6
 Method BLASTX

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NCBI GI g733454
BLAST score 317
E value 4.0e-29
Match length 66
% identity 94
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 402118
Seq. ID LIB3431-050-P1-K1-D7
Method BLASTX
NCBI GI g5541681
BLAST score 225
E value 3.0e-18
Match length 165
% identity 39
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]

Seq. No. 402119
Seq. ID LIB3431-050-P1-K1-D8
Method BLASTX
NCBI GI g6015065
BLAST score 308
E value 9.0e-29
Match length 64
% identity 92
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_ (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 402120
Seq. ID LIB3431-050-P1-K1-E1
Method BLASTX
NCBI GI g1835731
BLAST score 357
E value 5.0e-34
Match length 81
% identity 89
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402121
Seq. ID LIB3431-050-P1-K1-E10
Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 1.0e-10
Match length 47
% identity 65
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402122
Seq. ID LIB3431-050-P1-K1-E2
Method BLASTX
NCBI GI g2346966
BLAST score 144
E value 8.0e-09
Match length 57
% identity 53

NCBI Description (AB004871) CPC [Arabidopsis thaliana]
>gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative
DNA binding protein CPC [Arabidopsis thaliana]

Seq. No. 402123
Seq. ID LIB3431-050-P1-K1-E4
Method BLASTX
NCBI GI g3915186
BLAST score 231
E value 4.0e-19
Match length 86
% identity 55
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN
LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi_3128447
(AF061604) ubiquitin-conjugating enzyme homolog peroxin 4
[Pichia angusta]

Seq. No. 402124
Seq. ID LIB3431-050-P1-K1-E7
Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402125
Seq. ID LIB3431-050-P1-K1-E9
Method BLASTX
NCBI GI g3036946
BLAST score 281
E value 3.0e-25
Match length 56
% identity 95
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein
[Nicotiana glauca]

Seq. No. 402126
Seq. ID LIB3431-050-P1-K1-F1
Method BLASTX
NCBI GI g125580
BLAST score 155
E value 8.0e-11
Match length 48
% identity 73
NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
(PRK) >gi_100839_pir_S15743 phosphoribulokinase (EC
2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608)
phosphoribulokinase [Triticum aestivum]

Seq. No. 402127
Seq. ID LIB3431-050-P1-K1-F11
Method BLASTX
NCBI GI g4572679
BLAST score 161
E value 2.0e-11


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Match length      65
% identity        52
NCBI Description  (AC006954) RSZp22 splicing factor; contains RNA recognition
                  motif [Arabidopsis thaliana]
```

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Seq. No.          402128
Seq. ID           LIB3431-050-P1-K1-F3
Method            BLASTX
NCBI GI           g1172558
BLAST score       201
E value           7.0e-16
Match length      79
% identity        47
NCBI Description   OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
                  ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  >gi_480122_pir_S36454 porin por1 - garden pea
                  >qi_396819_emb_CAA80988 (Z25540) Porin [Pisum sativum]

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Seq. No.          402129
Seq. ID           LIB3431-050-P1-K1-F4
Method            BLASTX
NCBI GI           g115787
BLAST score       344
E value           1.0e-32
Match length      80
% identity        91
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

Seq. No.	402130
Seq. ID	LIB3431-050-P1-K1-F6
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	4.0e-11
Match length	36
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

```
Seq. No.      402131
Seq. ID      LIB3431-050-P1-K1-F8
Method       BLASTX
NCBI GI      g3688182
BLAST score   367
E value      2.0e-37
Match length  92
% identity    89
NCBI Description (AL031804) P-Protein - like protein [Arabidopsis thaliana]
```

```
Seq. No.      402132
Seq. ID      LIB3431-050-P1-K1-F9
Method       BLASTX
NCBI GI      g3789952
BLAST score  497
```

E value 2.0e-50
 Match length 102
 % identity 96
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 402133
 Seq. ID LIB3431-050-P1-K1-G1
 Method BLASTN
 NCBI GI g6006355
 BLAST score 125
 E value 8.0e-64
 Match length 260
 % identity 100
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 402134
 Seq. ID LIB3431-050-P1-K1-G10
 Method BLASTX
 NCBI GI g4680501
 BLAST score 216
 E value 2.0e-17
 Match length 91
 % identity 52
 NCBI Description (AF119222) hypothetical protein [Oryza sativa]

Seq. No. 402135
 Seq. ID LIB3431-050-P1-K1-G11
 Method BLASTX
 NCBI GI g21693
 BLAST score 450
 E value 5.0e-45
 Match length 83
 % identity 92
 NCBI Description (X66012) cathepsin B [Triticum aestivum]

Seq. No. 402136
 Seq. ID LIB3431-050-P1-K1-G4
 Method BLASTN
 NCBI GI g4959460
 BLAST score 38
 E value 9.0e-12
 Match length 38
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 402137
 Seq. ID LIB3431-050-P1-K1-G5
 Method BLASTX
 NCBI GI g3687440
 BLAST score 310
 E value 1.0e-28
 Match length 107
 % identity 54
 NCBI Description (AL022577) dJ353H6.2.1 (SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1)) [Homo sapiens]

Seq. No. 402138
 Seq. ID LIB3431-050-P1-K1-G7
 Method BLASTX
 NCBI GI g417260
 BLAST score 349
 E value 5.0e-33
 Match length 110
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402139
 Seq. ID LIB3431-050-P1-K1-G8
 Method BLASTX
 NCBI GI g1944407
 BLAST score 265
 E value 3.0e-23
 Match length 65
 % identity 72
 NCBI Description (D86988) KIAA0221 [Homo sapiens]

Seq. No. 402140
 Seq. ID LIB3431-050-P1-K1-H11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 233
 E value 2.0e-19
 Match length 44
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402141
 Seq. ID LIB3431-050-P1-K1-H2
 Method BLASTX
 NCBI GI g320618
 BLAST score 406
 E value 9.0e-40
 Match length 96
 % identity 80
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 402142
 Seq. ID LIB3431-050-P1-K1-H3
 Method BLASTX
 NCBI GI g430947
 BLAST score 390
 E value 6.0e-38
 Match length 104
 % identity 72

Seq. No. 402147
 Seq. ID LIB3431-050-P1-N1-A2
 Method BLASTX
 NCBI GI g347451
 BLAST score 291
 E value 4.0e-26
 Match length 57
 % identity 98
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 402148
 Seq. ID LIB3431-050-P1-N1-A6
 Method BLASTX
 NCBI GI g2072555
 BLAST score 279
 E value 1.0e-24
 Match length 54
 % identity 93
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402149
 Seq. ID LIB3431-050-P1-N1-A9
 Method BLASTX
 NCBI GI g2499417
 BLAST score 277
 E value 1.0e-24
 Match length 62
 % identity 82
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
 >gi_1085826_pir_S49248 H-protein - Flaveria anomala
 >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 402150
 Seq. ID LIB3431-050-P1-N1-B10
 Method BLASTN
 NCBI GI g20262
 BLAST score 146
 E value 2.0e-76
 Match length 274
 % identity 89
 NCBI Description O.sativa light-induced mRNA

Seq. No. 402151
 Seq. ID LIB3431-050-P1-N1-B11
 Method BLASTX
 NCBI GI g4587570
 BLAST score 144
 E value 8.0e-09
 Match length 66
 % identity 45
 NCBI Description (AC006550) Strong similarity to gi_2244833 centromere protein homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from

this gene

Seq. No. 402152
Seq. ID LIB3431-050-P1-N1-B2
Method BLASTX
NCBI GI g115787
BLAST score 480
E value 3.0e-48
Match length 92
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2' PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402153
Seq. ID LIB3431-050-P1-N1-B5
Method BLASTX
NCBI GI g1429226
BLAST score 228
E value 1.0e-18
Match length 47
% identity 85
NCBI Description (X98861) TFIIA [Arabidopsis thaliana]

Seq. No. 402154
Seq. ID LIB3431-050-P1-N1-B8
Method BLASTX
NCBI GI g5729802
BLAST score 452
E value 6.0e-45
Match length 91
% identity 89
NCBI Description similar to S. pombe dim1+ >gi_2565275 (AF023611) Dim1p homolog [Homo sapiens]

Seq. No. 402155
Seq. ID LIB3431-050-P1-N1-C1
Method BLASTX
NCBI GI g3236242
BLAST score 334
E value 4.0e-31
Match length 98
% identity 69
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 402156
Seq. ID LIB3431-050-P1-N1-C11
Method BLASTX
NCBI GI g131176
BLAST score 203
E value 6.0e-16
Match length 47
% identity 87
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

BLAST score 150
E value 8.0e-79
Match length 250
% identity 91
NCBI Description Oryza sativa CatC gene for catalase, complete cds

Seq. No. 402162
Seq. ID LIB3431-050-P1-N1-D10
Method BLASTN
NCBI GI g3789949
BLAST score 186
E value 1.0e-100
Match length 298
% identity 91
NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No. 402163
Seq. ID LIB3431-050-P1-N1-D11
Method BLASTX
NCBI GI g2072555
BLAST score 333
E value 5.0e-31
Match length 62
% identity 97
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402164
Seq. ID LIB3431-050-P1-N1-D4
Method BLASTX
NCBI GI g4680212
BLAST score 187
E value 7.0e-14
Match length 53
% identity 66
NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]

Seq. No. 402165
Seq. ID LIB3431-050-P1-N1-D7
Method BLASTX
NCBI GI g5541681
BLAST score 212
E value 7.0e-17
Match length 92
% identity 55
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]

Seq. No. 402166
Seq. ID LIB3431-050-P1-N1-E1
Method BLASTX
NCBI GI g1835731
BLAST score 187
E value 1.0e-28
Match length 88
% identity 80

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402167
Seq. ID LIB3431-050-P1-N1-E5
Method BLASTN
NCBI GI g11957
BLAST score 323
E value 0.0e+00
Match length 431
% identity 99
NCBI Description Rice complete chloroplast genome

Seq. No. 402168
Seq. ID LIB3431-050-P1-N1-E9
Method BLASTN
NCBI GI g20181
BLAST score 43
E value 6.0e-15
Match length 146
% identity 82
NCBI Description Rice cab2R gene for light harvesting chlorophyll
a/b-binding protein

Seq. No. 402169
Seq. ID LIB3431-050-P1-N1-F1
Method BLASTX
NCBI GI g21839
BLAST score 340
E value 8.0e-32
Match length 73
% identity 93
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402170
Seq. ID LIB3431-050-P1-N1-F12
Method BLASTN
NCBI GI g3273244
BLAST score 46
E value 1.0e-16
Match length 62
% identity 94
NCBI Description Oryza sativa DNA for NLS receptor, complete cds

Seq. No. 402171
Seq. ID LIB3431-050-P1-N1-F3
Method BLASTX
NCBI GI g1172555
BLAST score 184
E value 2.0e-13
Match length 61
% identity 57
NCBI Description 34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
(POM 34) >gi_629720_pir_S46936 34K porin - potato
>gi_1076682_pir_A55364 porin (clone pPOM-34) - potato
mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDa
porin [Solanum tuberosum]

BLAST score 38
 E value 5.0e-12
 Match length 42
 % identity 98
 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 402178
 Seq. ID LIB3431-050-P1-N1-H2
 Method BLASTX
 NCBI GI g421916
 BLAST score 168
 E value 1.0e-11
 Match length 31
 % identity 100
 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
 >gi_12582_emb_CAA48410_ (X68333) light harvesting
 chlorophyll a/b binding protein [Hedera helix]

Seq. No. 402179
 Seq. ID LIB3431-050-P1-N1-H4
 Method BLASTN
 NCBI GI g218207
 BLAST score 72
 E value 3.0e-32
 Match length 174
 % identity 85
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS1139

Seq. No. 402180
 Seq. ID LIB3431-050-P1-N1-H5
 Method BLASTN
 NCBI GI g2570514
 BLAST score 240
 E value 1.0e-132
 Match length 335
 % identity 93
 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 402181
 Seq. ID LIB3431-050-P1-N1-H9
 Method BLASTN
 NCBI GI g2072554
 BLAST score 135
 E value 6.0e-70
 Match length 183
 % identity 93
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 402182
 Seq. ID LIB3431-051-P1-K1-A11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 313
 E value 8.0e-29

Match length 62
 % identity 90
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402183
 Seq. ID LIB3431-051-P1-K1-A3
 Method BLASTN
 NCBI GI g20177
 BLAST score 102
 E value 2.0e-50
 Match length 123
 % identity 98
 NCBI Description Rice cab1R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 402184
 Seq. ID LIB3431-051-P1-K1-A5
 Method BLASTX
 NCBI GI g5103807
 BLAST score 349
 E value 5.0e-33
 Match length 93
 % identity 69
 NCBI Description (AC007591) Contains similarity to gb_AF014403 type-2
 phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo
 sapiens. ESTs gb_T88254 and gb_AA394650 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 402185
 Seq. ID LIB3431-051-P1-K1-A6
 Method BLASTN
 NCBI GI g5456937
 BLAST score 54
 E value 1.0e-21
 Match length 54
 % identity 100
 NCBI Description Oryza sativa rps9 mRNA for ribosomal protein S9, complete
 cds

Seq. No. 402186
 Seq. ID LIB3431-051-P1-K1-A9
 Method BLASTX
 NCBI GI g3885886
 BLAST score 642
 E value 2.0e-67
 Match length 125
 % identity 100
 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402187
 Seq. ID LIB3431-051-P1-K1-B1
 Method BLASTX
 NCBI GI g3913018
 BLAST score 494
 E value 5.0e-50

Match length	101
% identity	99
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]
Seq. No.	402188
Seq. ID	LIB3431-051-P1-K1-B12
Method	BLASTX
NCBI GI	g733454
BLAST score	450
E value	8.0e-45
Match length	108
% identity	80
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]
Seq. No.	402189
Seq. ID	LIB3431-051-P1-K1-B2
Method	BLASTX
NCBI GI	g2407281
BLAST score	517
E value	1.0e-52
Match length	107
% identity	93
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]
Seq. No.	402190
Seq. ID	LIB3431-051-P1-K1-B3
Method	BLASTX
NCBI GI	g3126854
BLAST score	534
E value	8.0e-55
Match length	102
% identity	96
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	402191
Seq. ID	LIB3431-051-P1-K1-B6
Method	BLASTX
NCBI GI	g606817
BLAST score	489
E value	2.0e-49
Match length	93
% identity	99
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]
Seq. No.	402192
Seq. ID	LIB3431-051-P1-K1-B7
Method	BLASTN
NCBI GI	g2624327
BLAST score	141
E value	2.0e-73
Match length	201

09584016-101000

% identity 93
NCBI Description Oryza sativa mRNA for glycine rich RNA-binding protein 2 (OsGRP2)

Seq. No. 402193
Seq. ID LIB3431-051-P1-K1-B8
Method BLASTX
NCBI GI g2499932
BLAST score 479
E value 2.0e-48
Match length 105
% identity 87
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305 (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]

Seq. No. 402194
Seq. ID LIB3431-051-P1-K1-C1
Method BLASTX
NCBI GI g2982453
BLAST score 474
E value 9.0e-48
Match length 109
% identity 83
NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No. 402195
Seq. ID LIB3431-051-P1-K1-C10
Method BLASTX
NCBI GI g124224
BLAST score 511
E value 9.0e-55
Match length 121
% identity 90
NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir_S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiation factor 5A (3) [Nicotiana tabacum]

Seq. No. 402196
Seq. ID LIB3431-051-P1-K1-C11
Method BLASTX
NCBI GI g2492514
BLAST score 525
E value 1.0e-53
Match length 110
% identity 94
NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No. 402197
Seq. ID LIB3431-051-P1-K1-C12
Method BLASTX
NCBI GI g115825
BLAST score 272


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BLAST score      160
E value         6.0e-11
Match length    31
% identity      87
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi_16471_emb_CAA32429 (X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]

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Seq. No.      402208
Seq. ID      LIB3431-051-P1-K1-D6
Method       BLASTX
NCBI GI      g2072555
BLAST score   150
E value      3.0e-10
Match length  30
% identity    90
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
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Seq. No.      402209
Seq. ID      LIB3431-051-P1-K1-D7
Method       BLASTN
NCBI GI      g3377792
BLAST score   106
E value      2.0e-52
Match length  309
% identity    84
NCBI Description  Oryza sativa ribulose-1,5-bisphosphate
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
```

```
Seq. No.      402210
Seq. ID       LIB3431-051-P1-K1-D8
Method        BLASTN
NCBI GI       g3821780
BLAST score   36
E value       1.0e-10
Match length  47
% identity    66
NCBI Description  Xenopus laevis cDNA clone 27A6-1
```

```
Seq. No.      402211
Seq. ID      LIB3431-051-P1-K1-D9
Method       BLASTX
NCBI GI      g131388
BLAST score   264
E value      5.0e-23
Match length  108
% identity    60
NCBI Description  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
photosystem II oxygen-evolving complex protein 1 - common
wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
```


NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 91R PRECURSOR (LHCII TYPE I CAB-91R) (LHCP) >gi_72732_pir_CDPJ91 chlorophyll a/b-binding protein 91R precursor - petunia
>gi_20487_emb_CAA26209_(X02356) cab 91R precursor polypeptide (aa -34 to 233) [Petunia sp.]

Seq. No. 402222
Seq. ID LIB3431-051-P1-K1-F10
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_(AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402223
Seq. ID LIB3431-051-P1-K1-F11
Method BLASTX
NCBI GI g320618
BLAST score 542
E value 2.0e-56
Match length 133
% identity 86
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_(D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 402224
Seq. ID LIB3431-051-P1-K1-F3
Method BLASTN
NCBI GI g3789951
BLAST score 254
E value 1.0e-141
Match length 297
% identity 97
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 402225
Seq. ID LIB3431-051-P1-K1-F4
Method BLASTX
NCBI GI g3913018
BLAST score 565
E value 2.0e-58
Match length 116
% identity 94
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_(D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 402226

Seq. ID	LIB3431-051-P1-K1-F7
Method	BLASTX
NCBI GI	g4582787
BLAST score	373
E value	5.0e-36
Match length	96
% identity	79
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

```
Seq. No.          402227
Seq. ID           LIB3431-051-P1-K1-F8
Method            BLASTX
NCBI GI           g115813
BLAST score       304
E value           1.0e-27
Match length      93
% identity        69
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
```

```
Seq. No.      402228
Seq. ID      LIB3431-051-P1-K1-F9
Method       BLASTX
NCBI GI      g2306981
BLAST score   170
E value      3.0e-12
Match length  78
% identity    45
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
```

```
Seq. No.      402229
Seq. ID      LIB3431-051-P1-K1-G1
Method       BLASTX
NCBI GI      g3126854
BLAST score   348
E value      5.0e-33
Match length  69
% identity    97
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      402230
Seq. ID      LIB3431-051-P1-K1-G10
Method       BLASTX
NCBI GI      g4091129
BLAST score   198
E value      4.0e-15
Match length  154
% identity    31
NCBI Description (AF050165) protein phosphatase 2A regulatory subunit PR59;
                PP2A regulatory subunit PR59 [Mus musculus]
```

```
Seq. No.      402231
Seq. ID      LIB3431-051-P1-K1-G11
Method       BLASTX
NCBI GI      g3126854
BLAST score   541
```

E value 2.0e-55
 Match length 112
 % identity 92
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402232
 Seq. ID LIB3431-051-P1-K1-G12
 Method BLASTX
 NCBI GI g132105
 BLAST score 268
 E value 9.0e-43
 Match length 109
 % identity 82
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402233
 Seq. ID LIB3431-051-P1-K1-G3
 Method BLASTX
 NCBI GI g5523862
 BLAST score 367
 E value 3.0e-35
 Match length 99
 % identity 69
 NCBI Description (AF085169) LRk-type protein [Triticum aestivum]

Seq. No. 402234
 Seq. ID LIB3431-051-P1-K1-G4
 Method BLASTX
 NCBI GI g3789954
 BLAST score 458
 E value 1.0e-45
 Match length 109
 % identity 83
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 402235
 Seq. ID LIB3431-051-P1-K1-G5
 Method BLASTX
 NCBI GI g82080
 BLAST score 230
 E value 3.0e-19
 Match length 76
 % identity 63
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 402236

light-regulated gene [Oryza sativa]

Seq. No. 402241
 Seq. ID LIB3431-051-P1-K1-H4
 Method BLASTN
 NCBI GI g3345476
 BLAST score 260
 E value 1.0e-144
 Match length 282
 % identity 99
 NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 402242
 Seq. ID LIB3431-051-P1-K1-H7
 Method BLASTX
 NCBI GI g4678947
 BLAST score 353
 E value 2.0e-33
 Match length 101
 % identity 65
 NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No. 402243
 Seq. ID LIB3431-051-P1-N1-A1
 Method BLASTX
 NCBI GI g1170606
 BLAST score 159
 E value 1.0e-10
 Match length 49
 % identity 65
 NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
 >gi_629863_pir_S45634 adenylate kinase (EC 2.7.4.3),
 chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A,
 Adenylate Kinase From Maize In Complex With The Inhibitor
 P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)
 >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize
 In Complex With The Inhibitor
 P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No. 402244
 Seq. ID LIB3431-051-P1-N1-A10
 Method BLASTN
 NCBI GI g2072554
 BLAST score 164
 E value 4.0e-87
 Match length 296
 % identity 89
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 402245
 Seq. ID LIB3431-051-P1-N1-A12
 Method BLASTX
 NCBI GI g2864617
 BLAST score 179
 E value 4.0e-13
 Match length 60

% identity 65
 NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1 (AJ245574) ATP synthase beta chain precursor (subunit II) [Arabidopsis thaliana]

Seq. No. 402246
 Seq. ID LIB3431-051-P1-N1-A2
 Method BLASTX
 NCBI GI g693920
 BLAST score 356
 E value 8.0e-34
 Match length 68
 % identity 100
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No. 402247
 Seq. ID LIB3431-051-P1-N1-A5
 Method BLASTN
 NCBI GI g5456937
 BLAST score 329
 E value 0.0e+00
 Match length 329
 % identity 100
 NCBI Description Oryza sativa rps9 mRNA for ribosomal protein S9, complete cds

Seq. No. 402248
 Seq. ID LIB3431-051-P1-N1-A6
 Method BLASTX
 NCBI GI g4508079
 BLAST score 350
 E value 4.0e-33
 Match length 95
 % identity 66
 NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 402249
 Seq. ID LIB3431-051-P1-N1-A9
 Method BLASTN
 NCBI GI g18266
 BLAST score 35
 E value 3.0e-10
 Match length 47
 % identity 94
 NCBI Description C.stellata mRNA for ribosomal protein L27

Seq. No. 402250
 Seq. ID LIB3431-051-P1-N1-B1
 Method BLASTX
 NCBI GI g132105
 BLAST score 537
 E value 5.0e-55
 Match length 99
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

09634016 101000

```
Seq. No.      402252
Seq. ID      LIB3431-051-P1-N1-B11
Method       BLASTX
NCBI GI      g4538963
BLAST score   169
E value      5.0e-12
Match length  48
% identity    71
NCBI Description (AL049488) chlorophyll a/b-binding protein-like
               [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
               (AF134129) Lhcb5 protein [Arabidopsis thaliana]
```

```
Seq. No.      402254
Seq. ID       LIB3431-05i-P1-N1-B4
Method        BLASTN
NCBI GI       g2072554
BLAST score    134
E value       4.0e-69
Match length   354
% identity     85
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds
```

51652

NCBI GI g3345477
 BLAST score 172
 E value 3.0e-12
 Match length 32
 % identity 97
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402256
 Seq. ID LIB3431-051-P1-N1-B6
 Method BLASTN
 NCBI GI g2624327
 BLAST score 240
 E value 1.0e-132
 Match length 284
 % identity 96
 NCBI Description Oryza sativa mRNA for glycine rich RNA-binding protein 2 (OsGRP2)

Seq. No. 402257
 Seq. ID LIB3431-051-P1-N1-B8
 Method BLASTX
 NCBI GI g2440046
 BLAST score 163
 E value 3.0e-11
 Match length 40
 % identity 70
 NCBI Description (AJ001294) major intrinsic protein PIPC [Craterostigma plantagineum]

Seq. No. 402258
 Seq. ID LIB3431-051-P1-N1-C1
 Method BLASTN
 NCBI GI g20191
 BLAST score 215
 E value 1.0e-117
 Match length 279
 % identity 94
 NCBI Description O.sativa mRNA for catalase

Seq. No. 402259
 Seq. ID LIB3431-051-P1-N1-C10
 Method BLASTX
 NCBI GI g5734790
 BLAST score 373
 E value 9.0e-36
 Match length 80
 % identity 90
 NCBI Description (AC007980) ATP-dependent metalloprotease [Arabidopsis thaliana]

Seq. No. 402260
 Seq. ID LIB3431-051-P1-N1-C11
 Method BLASTN
 NCBI GI g20177
 BLAST score 44
 E value 7.0e-16
 Match length 88

[Zea mays]

Seq. No. 402266
Seq. ID LIB3431-051-P1-N1-D11
Method BLASTX
NCBI GI g5106775
BLAST score 363
E value 1.0e-34
Match length 71
% identity 96
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No. 402267
Seq. ID LIB3431-051-P1-N1-D12
Method BLASTX
NCBI GI g5106775
BLAST score 259
E value 2.0e-22
Match length 52
% identity 92
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No. 402268
Seq. ID LIB3431-051-P1-N1-D4
Method BLASTX
NCBI GI g132166
BLAST score 160
E value 5.0e-11
Match length 31
% identity 87
NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
>gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
activase precursor - Arabidopsis thaliana
>gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -
473) [Arabidopsis thaliana]

Seq. No. 402269
Seq. ID LIB3431-051-P1-N1-D5
Method BLASTX
NCBI GI g167097
BLAST score 142
E value 7.0e-09
Match length 30
% identity 83
NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
[Hordeum vulgare]

Seq. No. 402270
Seq. ID LIB3431-051-P1-N1-D6
Method BLASTN
NCBI GI g3377792
BLAST score 97
E value 4.0e-47
Match length 267
% identity 84
NCBI Description Oryza sativa ribulose-1,5-bisphosphate

carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 402271
 Seq. ID LIB3431-051-P1-N1-D8
 Method BLASTN
 NCBI GI g416266
 BLAST score 211
 E value 1.0e-115
 Match length 269
 % identity 94
 NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence

Seq. No. 402272
 Seq. ID LIB3431-051-P1-N1-D9
 Method BLASTX
 NCBI GI g733454
 BLAST score 158
 E value 8.0e-11
 Match length 45
 % identity 69
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 402273
 Seq. ID LIB3431-051-P1-N1-E1
 Method BLASTX
 NCBI GI g2961176
 BLAST score 322
 E value 7.0e-30
 Match length 81
 % identity 80
 NCBI Description (AF050674) ribosomal protein L27 precursor [Oryza sativa]

Seq. No. 402274
 Seq. ID LIB3431-051-P1-N1-E10
 Method BLASTX
 NCBI GI g3928140
 BLAST score 166
 E value 1.0e-11
 Match length 34
 % identity 88
 NCBI Description (AJ131044) chlorophyll a/b binding protein [Cicer arietinum]

Seq. No. 402275
 Seq. ID LIB3431-051-P1-N1-E5
 Method BLASTX
 NCBI GI g1070408
 BLAST score 166
 E value 1.0e-11
 Match length 47
 % identity 74
 NCBI Description ferredoxin [2Fe-2S] I - rice

Seq. No. 402276
 Seq. ID LIB3431-051-P1-N1-E7
 Method BLASTX

NCBI GI g115786
 BLAST score 202
 E value 8.0e-16
 Match length 52
 % identity 75
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 402277
 Seq. ID LIB3431-051-P1-N1-E9
 Method BLASTN
 NCBI GI g5917782
 BLAST score 139
 E value 2.0e-72
 Match length 228
 % identity 89
 NCBI Description Oryza sativa carbonic anhydrase 3 mRNA, complete cds

Seq. No. 402278
 Seq. ID LIB3431-051-P1-N1-F10
 Method BLASTX
 NCBI GI g3036949
 BLAST score 262
 E value 7.0e-23
 Match length 53
 % identity 94
 NCBI Description (AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 402279
 Seq. ID LIB3431-051-P1-N1-F2
 Method BLASTN
 NCBI GI g3789951
 BLAST score 136
 E value 2.0e-70
 Match length 311
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 402280
 Seq. ID LIB3431-051-P1-N1-F8
 Method BLASTX
 NCBI GI g551047
 BLAST score 241
 E value 2.0e-20
 Match length 50
 % identity 90
 NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 402281
 Seq. ID LIB3431-051-P1-N1-F9
 Method BLASTN
 NCBI GI g2306980

```
BLAST score      180
E value         9.0e-97
Match length    240
% identity      94
NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                  complete cds
```

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Seq. No.      402282
Seq. ID      LIB3431-051-P1-N1-G10
Method       BLASTX
NCBI GI      g3126854
BLAST score   270
E value      1.0e-23
Match length  52
% identity    98
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      402283
Seq. ID       LIB3431-051-P1-N1-G11
Method        BLASTX
NCBI GI       g671740
BLAST score    170
E value       5.0e-12
Match length   41
% identity     83
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

```
Seq. No.          402284
Seq. ID           LIB3431-051-P1-N1-G12
Method            BLASTX
NCBI GI           g132105
BLAST score       167
E value           1.0e-11
Match length      33
% identity        97
NCBI Description  RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.      402285
Seq. ID       LIB3431-051-P1-N1-G2
Method        BLASTX
NCBI GI       g5679314
BLAST score   317
E value       3.0e-29
Match length  100
% identity    66
NCBI Description (AF164021) receptor kinase [Oryza sativa]
```

Seq. No. 402286

09684016.101000

Seq. ID	LIB3431-051-P1-N1-G3
Method	BLASTN
NCBI GI	g3789953
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	402287
Seq. ID	LIB3431-051-P1-N1-G6
Method	BLASTX
NCBI GI	g1617197
BLAST score	225
E value	2.0e-18
Match length	47
% identity	87
NCBI Description	(272488) CP12 [Nicotiana tabacum]
Seq. No.	402288
Seq. ID	LIB3431-051-P1-N1-G8
Method	BLASTN
NCBI GI	g20369
BLAST score	292
E value	1.0e-163
Match length	308
% identity	99
NCBI Description	Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31) >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase
Seq. No.	402289
Seq. ID	LIB3431-051-P1-N1-H1
Method	BLASTN
NCBI GI	g1519250
BLAST score	385
E value	0.0e+00
Match length	421
% identity	98
NCBI Description	Oryza sativa GF14-c protein mRNA, complete cds
Seq. No.	402290
Seq. ID	LIB3431-051-P1-N1-H10
Method	BLASTX
NCBI GI	g133936
BLAST score	610
E value	1.0e-63
Match length	125
% identity	97
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir_R3RZ3 ribosomal protein S3 - rice chloroplast >gi_12025_emb_CAA33934_(X15901) ribosomal protein S3 [Oryza sativa] >gi_226646_prf_1603356BW ribosomal protein S3 [Oryza sativa]

thaliana]

Seq. No. 402296
 Seq. ID LIB3431-052-P1-K1-A12
 Method BLASTN
 NCBI GI g6015437
 BLAST score 41
 E value 6.0e-14
 Match length 52
 % identity 68
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402297
 Seq. ID LIB3431-052-P1-K1-A4
 Method BLASTX
 NCBI GI g131225
 BLAST score 308
 E value 2.0e-28
 Match length 70
 % identity 87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402298
 Seq. ID LIB3431-052-P1-K1-A8
 Method BLASTX
 NCBI GI g168643
 BLAST score 260
 E value 7.0e-23
 Match length 83
 % identity 65
 NCBI Description (L02540) NADPH HC-toxin reductase [Zea mays]

Seq. No. 402299
 Seq. ID LIB3431-052-P1-K1-B11
 Method BLASTN
 NCBI GI g2062705
 BLAST score 36
 E value 9.0e-11
 Match length 36
 % identity 100
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 402300
 Seq. ID LIB3431-052-P1-K1-B12
 Method BLASTX
 NCBI GI g3158476
 BLAST score 230
 E value 2.0e-19
 Match length 62
 % identity 71
 NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 402301
 Seq. ID LIB3431-052-P1-K1-B4

NCBI GI g3789952
 BLAST score 341
 E value 5.0e-32
 Match length 66
 % identity 98
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 402326
 Seq. ID LIB3431-052-P1-K1-F2
 Method BLASTX
 NCBI GI g3075488
 BLAST score 303
 E value 9.0e-28
 Match length 82
 % identity 72
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402327
 Seq. ID LIB3431-052-P1-K1-F4
 Method BLASTN
 NCBI GI g4959460
 BLAST score 33
 E value 3.0e-09
 Match length 33
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 402328
 Seq. ID LIB3431-052-P1-K1-F5
 Method BLASTX
 NCBI GI g3360289
 BLAST score 230
 E value 4.0e-19
 Match length 59
 % identity 76
 NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No. 402329
 Seq. ID LIB3431-052-P1-K1-F7
 Method BLASTX
 NCBI GI g5302772
 BLAST score 148
 E value 1.0e-09
 Match length 83
 % identity 40
 NCBI Description (Z97336) SNF1 like protein kinase [Arabidopsis thaliana]

Seq. No. 402330
 Seq. ID LIB3431-052-P1-K1-F8
 Method BLASTX
 NCBI GI g2129622
 BLAST score 296
 E value 5.0e-27
 Match length 71
 % identity 77

NCBI GI g6056418
 BLAST score 287
 E value 1.0e-25
 Match length 94
 % identity 59
 NCBI Description (AC009525) Similar to beta-glucosidases [Arabidopsis thaliana]

Seq. No. 402355
 Seq. ID LIB3431-052-P1-N1-C12
 Method BLASTX
 NCBI GI g3328221
 BLAST score 443
 E value 7.0e-44
 Match length 96
 % identity 89
 NCBI Description (AF076920) thioredoxin peroxidase [Secale cereale]

Seq. No. 402356
 Seq. ID LIB3431-052-P1-N1-C2
 Method BLASTX
 NCBI GI g2982456
 BLAST score 312
 E value 2.0e-28
 Match length 90
 % identity 68
 NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 402357
 Seq. ID LIB3431-052-P1-N1-C3
 Method BLASTX
 NCBI GI g2754849
 BLAST score 280
 E value 9.0e-25
 Match length 65
 % identity 85
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No. 402358
 Seq. ID LIB3431-052-P1-N1-C4
 Method BLASTX
 NCBI GI g399333
 BLAST score 205
 E value 5.0e-16
 Match length 44
 % identity 89
 NCBI Description CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYL SERINE SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE) >gi_322740_pir_A43407 cysteine synthase (EC 4.2.99.8) precursor - pepper >gi_17944_emb_CAA46086_ (X64874) O-acetylserine (thiol)-lyase [Capsicum annuum]

Seq. No. 402359
 Seq. ID LIB3431-052-P1-N1-C5
 Method BLASTX
 NCBI GI g4566614

E value 8.0e-18
 Match length 55
 % identity 78
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 402365
 Seq. ID LIB3431-052-P1-N1-D6
 Method BLASTX
 NCBI GI g671740
 BLAST score 426
 E value 7.0e-42
 Match length 77
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402366
 Seq. ID LIB3431-052-P1-N1-D7
 Method BLASTX
 NCBI GI g4335763
 BLAST score 167
 E value 1.0e-11
 Match length 75
 % identity 45
 NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 402367
 Seq. ID LIB3431-052-P1-N1-D9
 Method BLASTX
 NCBI GI g4566614
 BLAST score 306
 E value 9.0e-28
 Match length 69
 % identity 84
 NCBI Description (AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No. 402368
 Seq. ID LIB3431-052-P1-N1-E1
 Method BLASTN
 NCBI GI g218207
 BLAST score 295
 E value 1.0e-165
 Match length 295
 % identity 100
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 402369
 Seq. ID LIB3431-052-P1-N1-E12
 Method BLASTX
 NCBI GI g3510256
 BLAST score 298
 E value 6.0e-27

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402375
Seq. ID LIB3431-052-P1-N1-E7
Method BLASTX
NCBI GI g671740
BLAST score 346
E value 9.0e-33
Match length 76
% identity 84
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402376
Seq. ID LIB3431-052-P1-N1-E9
Method BLASTX
NCBI GI g1173347
BLAST score 331
E value 1.0e-30
Match length 82
% identity 83
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 402377
Seq. ID LIB3431-052-P1-N1-F10
Method BLASTN
NCBI GI g3789951
BLAST score 77
E value 3.0e-35
Match length 245
% identity 82
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 402378
Seq. ID LIB3431-052-P1-N1-F11
Method BLASTX
NCBI GI g21839
BLAST score 343
E value 4.0e-32
Match length 72
% identity 94
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402379
Seq. ID LIB3431-052-P1-N1-F12
Method BLASTN
NCBI GI g21838
BLAST score 36
E value 1.0e-10
Match length 139

% identity 79
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 402385
 Seq. ID LIB3431-052-P1-N1-G3
 Method BLASTX
 NCBI GI g2501190
 BLAST score 470
 E value 5.0e-47
 Match length 117
 % identity 83
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 402386
 Seq. ID LIB3431-052-P1-N1-G8
 Method BLASTN
 NCBI GI g21838
 BLAST score 70
 E value 5.0e-31
 Match length 207
 % identity 85
 NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase

Seq. No. 402387
 Seq. ID LIB3431-052-P1-N1-G9
 Method BLASTX
 NCBI GI g693920
 BLAST score 403
 E value 4.0e-39
 Match length 77
 % identity 99
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum
 tuberosum]

Seq. No. 402388
 Seq. ID LIB3431-052-P1-N1-H1
 Method BLASTX
 NCBI GI g115787
 BLAST score 495
 E value 6.0e-50
 Match length 98
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 402389
 Seq. ID LIB3431-052-P1-N1-H10
 Method BLASTX
 NCBI GI g82080

BLAST score 291
 E value 4.0e-26
 Match length 71
 % identity 82
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 402390
 Seq. ID LIB3431-052-P1-N1-H11
 Method BLASTX
 NCBI GI g119194
 BLAST score 270
 E value 9.0e-24
 Match length 62
 % identity 85
 NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
 >gi_81607_pir_S09152 translation elongation factor Tu
 precursor, chloroplast - Arabidopsis thaliana
 >gi_22565_emb_CAA36498_(X52256) elongation factor Tu
 precursor [Arabidopsis thaliana]
 >gi_5738381_emb_CAB45802.2_(AL080253) translation
 elongation factor EF-Tu precursor, chloroplast [Arabidopsis
 thaliana] >gi_226817_prf_1607332A elongation factor Tu
 [Arabidopsis thaliana]

Seq. No. 402391
 Seq. ID LIB3431-052-P1-N1-H2
 Method BLASTX
 NCBI GI g226263
 BLAST score 158
 E value 1.0e-10
 Match length 29
 % identity 97
 NCBI Description chlorophyll a/b binding protein [Glycine max]

Seq. No. 402392
 Seq. ID LIB3431-052-P1-N1-H3
 Method BLASTX
 NCBI GI g3789954
 BLAST score 237
 E value 7.0e-20
 Match length 44
 % identity 95
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 402393
 Seq. ID LIB3431-052-P1-N1-H5
 Method BLASTN
 NCBI GI g14264
 BLAST score 60
 E value 5.0e-25
 Match length 100
 % identity 90
 NCBI Description T.aestivum gene for sedoheptulose-1,7-bisphosphatase

Seq. No. 402394
 Seq. ID LIB3431-052-P1-N1-H7
 Method BLASTX
 NCBI GI g131176
 BLAST score 251
 E value 1.0e-21
 Match length 48
 % identity 98
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
 >gi_72683_pir_F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No. 402395
 Seq. ID LIB3431-052-P1-N1-H9
 Method BLASTX
 NCBI GI g3183079
 BLAST score 209
 E value 1.0e-16
 Match length 54
 % identity 76
 NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
 >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No. 402396
 Seq. ID LIB3431-053-P1-K1-A1
 Method BLASTX
 NCBI GI g871931
 BLAST score 387
 E value 2.0e-37
 Match length 78
 % identity 99
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 402397
 Seq. ID LIB3431-053-P1-K1-A10
 Method BLASTX
 NCBI GI g729479
 BLAST score 667
 E value 1.0e-72
 Match length 147
 % identity 82
 NCBI Description FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No. 402398
 Seq. ID LIB3431-053-P1-K1-A11
 Method BLASTX
 NCBI GI g131225
 BLAST score 322
 E value 3.0e-30
 Match length 71
 % identity 87

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402399
 Seq. ID LIB3431-053-P1-K1-A12
 Method BLASTX
 NCBI GI g4585882
 BLAST score 638
 E value 8.0e-67
 Match length 143
 % identity 79
 NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 402400
 Seq. ID LIB3431-053-P1-K1-A2
 Method BLASTX
 NCBI GI g2894534
 BLAST score 392
 E value 4.0e-38
 Match length 103
 % identity 77
 NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 402401
 Seq. ID LIB3431-053-P1-K1-A3
 Method BLASTX
 NCBI GI g4038699
 BLAST score 198
 E value 3.0e-23
 Match length 65
 % identity 82
 NCBI Description (AB020947) ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Aegilops speltoides]

Seq. No. 402402
 Seq. ID LIB3431-053-P1-K1-A6
 Method BLASTX
 NCBI GI g417154
 BLAST score 429
 E value 3.0e-42
 Match length 135
 % identity 63
 NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 402403
 Seq. ID LIB3431-053-P1-K1-A7
 Method BLASTX
 NCBI GI g2407281
 BLAST score 399
 E value 5.0e-39
 Match length 81

Seq. No. 402413
 Seq. ID LIB3431-053-P1-K1-B9
 Method BLASTX
 NCBI GI g1835731
 BLAST score 319
 E value 1.0e-29
 Match length 66
 % identity 95
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402414
 Seq. ID LIB3431-053-P1-K1-C1
 Method BLASTX
 NCBI GI g5734636
 BLAST score 297
 E value 8.0e-27
 Match length 106
 % identity 50
 NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No. 402415
 Seq. ID LIB3431-053-P1-K1-C11
 Method BLASTX
 NCBI GI g2130042
 BLAST score 688
 E value 1.0e-72
 Match length 149
 % identity 92
 NCBI Description Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916) protoporphyrin IX Mg-chelatase subunit precursor [Hordeum vulgare]

Seq. No. 402416
 Seq. ID LIB3431-053-P1-K1-C12
 Method BLASTX
 NCBI GI g115772
 BLAST score 675
 E value 4.0e-71
 Match length 136
 % identity 94
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 402417
 Seq. ID LIB3431-053-P1-K1-C2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 194
 E value 6.0e-15
 Match length 52
 % identity 73
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

0964016 10000

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Seq. No.          402419
Seq. ID           LIB3431-053-P1-K1-C4
Method            BLASTN
NCBI GI           g6015437
BLAST score       36
E value           2.0e-10
Match length      36
% identity         100
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
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Seq. No.          402421
Seq. ID           LIB3431-053-P1-K1-C6
Method            BLASTX
NCBI GI           g82734
BLAST score       812
E value           4.0e-87
Match length      164
% identity        31
NCBI Description   ubiquitin precursor - maize (fragment)
                  >gi 226763 prf 1604470A poly-ubiquitin [Zea mays]
```

51686

Match length 102
 % identity 84
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 402423
 Seq. ID LIB3431-053-P1-K1-D10
 Method BLASTX
 NCBI GI g548605
 BLAST score 488
 E value 3.0e-49
 Match length 113
 % identity 87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 402424
 Seq. ID LIB3431-053-P1-K1-D12
 Method BLASTX
 NCBI GI g3288821
 BLAST score 422
 E value 2.0e-41
 Match length 106
 % identity 75
 NCBI Description (AF063901) alanine:glyoxylate aminotransferase;
 transaminase [Arabidopsis thaliana]
 >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
 alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 402425
 Seq. ID LIB3431-053-P1-K1-D2
 Method BLASTN
 NCBI GI g5852170
 BLAST score 86
 E value 2.0e-40
 Match length 130
 % identity 46
 NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
 clone:tl7804

Seq. No. 402426
 Seq. ID LIB3431-053-P1-K1-D3
 Method BLASTX
 NCBI GI g4972052
 BLAST score 372
 E value 1.0e-35
 Match length 134
 % identity 40
 NCBI Description (AL078470) putative protein [Arabidopsis thaliana]

Seq. No. 402427

NCBI GI g3885891
 BLAST score 171
 E value 2.0e-91
 Match length 209
 % identity 96
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 402433
 Seq. ID LIB3431-053-P1-K1-E11
 Method BLASTX
 NCBI GI g4544390
 BLAST score 364
 E value 1.0e-34
 Match length 141
 % identity 52
 NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402434
 Seq. ID LIB3431-053-P1-K1-E12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402435
 Seq. ID LIB3431-053-P1-K1-E2
 Method BLASTN
 NCBI GI g218209
 BLAST score 66
 E value 2.0e-28
 Match length 94
 % identity 93
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 402436
 Seq. ID LIB3431-053-P1-K1-E3
 Method BLASTX
 NCBI GI g2072727
 BLAST score 736
 E value 3.0e-78
 Match length 143
 % identity 99
 NCBI Description (Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No. 402437
 Seq. ID LIB3431-053-P1-K1-E4
 Method BLASTN
 NCBI GI g3821780
 BLAST score 35

E value 7.0e-11
 Match length 35
 % identity 100
 NCBI Description *Xenopus laevis* cDNA clone 27A6-1

Seq. No. 402438
 Seq. ID LIB3431-053-P1-K1-E5
 Method BLASTN
 NCBI GI g3821780
 BLAST score 35
 E value 8.0e-11
 Match length 35
 % identity 100
 NCBI Description *Xenopus laevis* cDNA clone 27A6-1

Seq. No. 402439
 Seq. ID LIB3431-053-P1-K1-E6
 Method BLASTX
 NCBI GI g131388
 BLAST score 403
 E value 3.0e-39
 Match length 131
 % identity 67
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670 (X57408)
 33kDa oxygen evolving protein of photosystem II [*Triticum aestivum*]

Seq. No. 402440
 Seq. ID LIB3431-053-P1-K1-E7
 Method BLASTX
 NCBI GI g4417296
 BLAST score 368
 E value 3.0e-35
 Match length 102
 % identity 68
 NCBI Description (AC007019) unknown protein [*Arabidopsis thaliana*]
 >gi_4587592_gb_AAD25820.1_AC007232_10 (AC007232) unknown protein [*Arabidopsis thaliana*]

Seq. No. 402441
 Seq. ID LIB3431-053-P1-K1-E9
 Method BLASTX
 NCBI GI g3885894
 BLAST score 463
 E value 2.0e-46
 Match length 104
 % identity 88
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [*Oryza sativa*]

Seq. No. 402442
 Seq. ID LIB3431-053-P1-K1-F1
 Method BLASTX
 NCBI GI g2570511

09684016-101000

dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 402447
Seq. ID LIB3431-053-P1-K1-F8
Method BLASTN
NCBI GI g4835587
BLAST score 67
E value 1.0e-29
Match length 67
% identity 100
NCBI Description Oryza sativa ONIT4 mRNA for nitrilase-like protein,
complete cds

Seq. No. 402448
Seq. ID LIB3431-053-P1-K1-F9
Method BLASTX
NCBI GI g733456
BLAST score 631
E value 6.0e-66
Match length 141
% identity 85
NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 402449
Seq. ID LIB3431-053-P1-K1-G1
Method BLASTX
NCBI GI g3047064
BLAST score 406
E value 1.0e-39
Match length 143
% identity 57
NCBI Description (AF058825) contains similarity to peptidyl-prolyl cis-trans
isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41
[Arabidopsis thaliana])

Seq. No. 402450
Seq. ID LIB3431-053-P1-K1-G10
Method BLASTX
NCBI GI g671740
BLAST score 338
E value 2.0e-31
Match length 63
% identity 98
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]

Seq. No. 402451
Seq. ID LIB3431-053-P1-K1-G11
Method BLASTX
NCBI GI g132105
BLAST score 653
E value 2.0e-68
Match length 141
% identity 88
NCBI Description RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402452
Seq. ID LIB3431-053-P1-K1-G2
Method BLASTN
NCBI GI g20262
BLAST score 340
E value 0.0e+00
Match length 340
% identity 100
NCBI Description O.sativa light-induced mRNA

Seq. No. 402453
Seq. ID LIB3431-053-P1-K1-G3
Method BLASTX
NCBI GI g3510256
BLAST score 250
E value 3.0e-21
Match length 118
% identity 47
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 402454
Seq. ID LIB3431-053-P1-K1-G4
Method BLASTX
NCBI GI g132105
BLAST score 525
E value 1.0e-53
Match length 117
% identity 85
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402455
Seq. ID LIB3431-053-P1-K1-G5
Method BLASTX
NCBI GI g132105
BLAST score 313
E value 6.0e-29
Match length 80
% identity 80
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

sequences; and unknown genes

Seq. No. 402460
Seq. ID LIB3431-053-P1-K1-H2
Method BLASTX
NCBI GI g733454
BLAST score 357
E value 6.0e-34
Match length 101
% identity 72
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 402461
Seq. ID LIB3431-053-P1-K1-H3
Method BLASTX
NCBI GI g4582459
BLAST score 329
E value 1.0e-30
Match length 98
% identity 63
NCBI Description (AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No. 402462
Seq. ID LIB3431-053-P1-K1-H6
Method BLASTX
NCBI GI g2570496
BLAST score 118
E value 1.0e-59
Match length 126
% identity 98
NCBI Description Oryza sativa H protein subunit of glycine decarboxylase mRNA, complete cds

Seq. No. 402463
Seq. ID LIB3431-053-P1-K1-H7
Method BLASTX
NCBI GI g5442410
BLAST score 380
E value 2.0e-36
Match length 133
% identity 58
NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 402464
Seq. ID LIB3431-053-P1-K1-H8
Method BLASTX
NCBI GI g2407281
BLAST score 661
E value 2.0e-69
Match length 129
% identity 94
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 402465

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Seq. ID      LIB3431-053-P1-K1-H9
Method       BLASTX
NCBI GI      g3789952
BLAST score   469
E value      4.0e-47
Match length  107
% identity    87
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
               sativa]
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Seq. No.      402466
Seq. ID       LIB3431-053-P1-N1-A1
Method        BLASTN
NCBI GI       g218209
BLAST score    214
E value       1.0e-117
Match length   302
% identity     93
NCBI Description  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
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Seq. No.          402467
Seq. ID           LIB3431-053-P1-N1-A10
Method            BLASTX
NCBI GI           g729477
BLAST score       498
E value           3.0e-50
Match length      110
% identity        84
NCBI Description  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
                  >gi_320548_pir_A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                  [Mesembryanthemum crystallinum] >gi_226768_prf_1604475A
                  ferredoxin NADP reductase [Mesembryanthemum crystallinum]
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Seq. No.      402468
Seq. ID      LIB3431-053-P1-N1-A11
Method       BLASTX
NCBI GI      g131225
BLAST score   179
E value      4.0e-13
Match length  48
% identity    69
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [Hordeum vulgare]
```

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Seq. No.          402469
Seq. ID           LIB3431-053-P1-N1-A12
Method            BLASTX
NCBI GI           g115813
BLAST score       211
E value           8.0e-25
Match length      82
```


Seq. No. 402474
 Seq. ID LIB3431-053-P1-N1-A9
 Method BLASTX
 NCBI GI g2407281
 BLAST score 266
 E value 2.0e-23
 Match length 67
 % identity 75
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza sativa*]

Seq. No. 402475
 Seq. ID LIB3431-053-P1-N1-B10
 Method BLASTX
 NCBI GI g3036942
 BLAST score 181
 E value 3.0e-13
 Match length 37
 % identity 89
 NCBI Description (AB012636) light harvesting chlorophyll a/b-binding protein [*Nicotiana sylvestris*]

Seq. No. 402476
 Seq. ID LIB3431-053-P1-N1-B11
 Method BLASTX
 NCBI GI g347451
 BLAST score 229
 E value 9.0e-19
 Match length 48
 % identity 92
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [*Oryza sativa*]

Seq. No. 402477
 Seq. ID LIB3431-053-P1-N1-B12
 Method BLASTX
 NCBI GI g115813
 BLAST score 212
 E value 8.0e-17
 Match length 75
 % identity 61
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [*Lycopersicon esculentum*]

Seq. No. 402478
 Seq. ID LIB3431-053-P1-N1-B2
 Method BLASTX
 NCBI GI g2499819
 BLAST score 215
 E value 1.0e-30
 Match length 73
 % identity 86
 NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir_S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [*Oryza sativa*] >gi_1711289_dbj_BAA06875_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 402479
 Seq. ID LIB3431-053-P1-N1-B3
 Method BLASTX
 NCBI GI g4982478
 BLAST score 168
 E value 1.0e-11
 Match length 47
 % identity 68
 NCBI Description (AF069441) putative leucyl tRNA synthetase [Arabidopsis thaliana]

Seq. No. 402480
 Seq. ID LIB3431-053-P1-N1-B4
 Method BLASTX
 NCBI GI g421916
 BLAST score 237
 E value 5.0e-20
 Match length 49
 % identity 90
 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
 >gi_12582_emb_CAA48410_ (X68333) light harvesting
 chlorophyll a /b binding protein [Hedera helix]

Seq. No. 402481
 Seq. ID LIB3431-053-P1-N1-B8
 Method BLASTX
 NCBI GI g400983
 BLAST score 250
 E value 3.0e-21
 Match length 70
 % identity 69
 NCBI Description 50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)
 >gi_279648_pir_R5SP11 ribosomal protein L11 precursor -
 spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein
 L11 [Spinacia oleracea]

Seq. No. 402482
 Seq. ID LIB3431-053-P1-N1-B9
 Method BLASTX
 NCBI GI g1835731
 BLAST score 230
 E value 5.0e-19
 Match length 55
 % identity 82
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402483
 Seq. ID LIB3431-053-P1-N1-C10
 Method BLASTX
 NCBI GI g687677
 BLAST score 235
 E value 1.0e-19
 Match length 51
 % identity 88
 NCBI Description (U19925) unknown [Arabidopsis thaliana]

Seq. No. 402484
 Seq. ID LIB3431-053-P1-N1-C11
 Method BLASTX
 NCBI GI g2130042
 BLAST score 317
 E value 3.0e-32
 Match length 100
 % identity 75
 NCBI Description Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916)
 protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
 vulgare]

Seq. No. 402485
 Seq. ID LIB3431-053-P1-N1-C12
 Method BLASTX
 NCBI GI g2645999
 BLAST score 219
 E value 8.0e-18
 Match length 56
 % identity 73
 NCBI Description (AF034631) chlorophyll a/b binding protein of LHCII type I
 precursor [Panax ginseng]

Seq. No. 402486
 Seq. ID LIB3431-053-P1-N1-C2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 217
 E value 2.0e-17
 Match length 44
 % identity 93
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402487
 Seq. ID LIB3431-053-P1-N1-C3
 Method BLASTX
 NCBI GI g671740
 BLAST score 245
 E value 1.0e-20
 Match length 49
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 402488
 Seq. ID LIB3431-053-P1-N1-C5
 Method BLASTX
 NCBI GI g1835731
 BLAST score 459
 E value 1.0e-45
 Match length 102
 % identity 86
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	402489
Seq. ID	LIB3431-053-P1-N1-C6
Method	BLASTX
NCBI GI	g170354
BLAST score	422
E value	2.0e-41
Match length	85
% identity	21
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.	402490
Seq. ID	LIB3431-053-P1-N1-C8
Method	BLASTX
NCBI GI	g289920
BLAST score	319
E value	2.0e-29
Match length	61
% identity	100
NCBI Description	(L07119) chlorophyll A/B binding protein [Gossypium hirsutum]
Seq. No.	402491
Seq. ID	LIB3431-053-P1-N1-D10
Method	BLASTN
NCBI GI	g304219
BLAST score	52
E value	2.0e-20
Match length	80
% identity	91
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds
Seq. No.	402492
Seq. ID	LIB3431-053-P1-N1-D12
Method	BLASTX
NCBI GI	g2754849
BLAST score	192
E value	2.0e-29
Match length	74
% identity	85
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]
Seq. No.	402493
Seq. ID	LIB3431-053-P1-N1-D8
Method	BLASTX
NCBI GI	g3789952
BLAST score	196
E value	7.0e-15
Match length	39
% identity	95
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]
Seq. No.	402494
Seq. ID	LIB3431-053-P1-N1-E1
Method	BLASTX

NCBI GI g3885892
 BLAST score 302
 E value 2.0e-27
 Match length 61
 % identity 95
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402495
 Seq. ID LIB3431-053-P1-N1-E10
 Method BLASTX
 NCBI GI g5734636
 BLAST score 187
 E value 6.0e-16
 Match length 87
 % identity 49
 NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No. 402496
 Seq. ID LIB3431-053-P1-N1-E11
 Method BLASTX
 NCBI GI g4544390
 BLAST score 188
 E value 6.0e-14
 Match length 62
 % identity 50
 NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402497
 Seq. ID LIB3431-053-P1-N1-E2
 Method BLASTN
 NCBI GI g218209
 BLAST score 58
 E value 1.0e-23
 Match length 94
 % identity 90
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone POSSS2106

Seq. No. 402498
 Seq. ID LIB3431-053-P1-N1-E3
 Method BLASTN
 NCBI GI g2072726
 BLAST score 460
 E value 0.0e+00
 Match length 491
 % identity 99
 NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 402499
 Seq. ID LIB3431-053-P1-N1-E6
 Method BLASTX
 NCBI GI g482311
 BLAST score 420
 E value 4.0e-41
 Match length 84

Method BLASTX
 NCBI GI g6063542
 BLAST score 198
 E value 7.0e-16
 Match length 45
 % identity 98
 NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 402510
 Seq. ID LIB3431-053-P1-N1-F8
 Method BLASTN
 NCBI GI g4835587
 BLAST score 154
 E value 6.0e-81
 Match length 166
 % identity 99
 NCBI Description Oryza sativa ONIT4 mRNA for nitrilase-like protein, complete cds

Seq. No. 402511
 Seq. ID LIB3431-053-P1-N1-F9
 Method BLASTX
 NCBI GI g733454
 BLAST score 240
 E value 2.0e-37
 Match length 90
 % identity 92
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 402512
 Seq. ID LIB3431-053-P1-N1-G1
 Method BLASTX
 NCBI GI g3047064
 BLAST score 374
 E value 9.0e-36
 Match length 90
 % identity 73
 NCBI Description (AF058825) contains similarity to peptidyl-prolyl cis-trans isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41 [Arabidopsis thaliana])

Seq. No. 402513
 Seq. ID LIB3431-053-P1-N1-G10
 Method BLASTX
 NCBI GI g132105
 BLAST score 156
 E value 1.0e-16
 Match length 47
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

[illegible][illegible]

100000

[illegible][illegible]

% identity 94
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 402524
Seq. ID LIB3431-053-P1-N1-H5
Method BLASTX
NCBI GI g131225
BLAST score 318
E value 3.0e-37
Match length 101
% identity 81
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402525
Seq. ID LIB3431-053-P1-N1-H6
Method BLASTX
NCBI GI g2499417
BLAST score 327
E value 2.0e-30
Match length 78
% identity 79
NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir_S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 402526
Seq. ID LIB3431-053-P1-N1-H7
Method BLASTX
NCBI GI g5442410
BLAST score 157
E value 1.0e-15
Match length 109
% identity 43
NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 402527
Seq. ID LIB3431-053-P1-N1-H8
Method BLASTX
NCBI GI g132081
BLAST score 170
E value 2.0e-15
Match length 53
% identity 84
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68093_pir_RKRZS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - rice >gi_20341_emb_CAA30393_ (X07515) ribulose bisphosphate carboxylase [Oryza sativa]

Seq. No. 402528
Seq. ID LIB3431-053-P1-N1-H9
Method BLASTN

09634016-101000

NCBI GI g3927827
BLAST score 195
E value 7.0e-15
Match length 115
% identity 42
NCBI Description (AC005727) osmotin-like protein precursor [Arabidopsis thaliana]

Seq. No. 402548
Seq. ID LIB3431-054-P1-K1-C2
Method BLASTX
NCBI GI g2306981
BLAST score 441
E value 9.0e-44
Match length 125
% identity 74
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 402549
Seq. ID LIB3431-054-P1-K1-C3
Method BLASTX
NCBI GI g417260
BLAST score 421
E value 2.0e-41
Match length 128
% identity 66
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
light-regulated gene [Oryza sativa]

Seq. No. 402550
Seq. ID LIB3431-054-P1-K1-C4
Method BLASTN
NCBI GI g3885891
BLAST score 245
E value 1.0e-135
Match length 245
% identity 100
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
mRNA, complete cds

Seq. No. 402551
Seq. ID LIB3431-054-P1-K1-C5
Method BLASTX
NCBI GI g2832672
BLAST score 160
E value 1.0e-10
Match length 33
% identity 97
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No. 402552
Seq. ID LIB3431-054-P1-K1-C6
Method BLASTN
NCBI GI g1835730
BLAST score 120
E value 5.0e-61

Match length 176
 % identity 92
 NCBI Description *Oryza sativa* photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 402553
 Seq. ID LIB3431-054-P1-K1-C7
 Method BLASTX
 NCBI GI g2924520
 BLAST score 609
 E value 3.0e-63
 Match length 159
 % identity 72
 NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP) [*Arabidopsis thaliana*]

Seq. No. 402554
 Seq. ID LIB3431-054-P1-K1-C8
 Method BLASTX
 NCBI GI g3789954
 BLAST score 628
 E value 1.0e-65
 Match length 159
 % identity 75
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [*Oryza sativa*]

Seq. No. 402555
 Seq. ID LIB3431-054-P1-K1-C9
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [*Oryza sativa*]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [*Oryza sativa*]

Seq. No. 402556
 Seq. ID LIB3431-054-P1-K1-D1
 Method BLASTN
 NCBI GI g2677829
 BLAST score 133
 E value 2.0e-68
 Match length 341
 % identity 85
 NCBI Description *Prunus armeniaca* ribosomal protein L12 mRNA, complete cds

Seq. No. 402557
 Seq. ID LIB3431-054-P1-K1-D10
 Method BLASTX
 NCBI GI g1778095
 BLAST score 452
 E value 4.0e-45
 Match length 122
 % identity 71

NCBI Description (U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No. 402558
Seq. ID LIB3431-054-P1-K1-D2
Method BLASTN
NCBI GI g4138289
BLAST score 192
E value 1.0e-104
Match length 251
% identity 94
NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 402559
Seq. ID LIB3431-054-P1-K1-D3
Method BLASTX
NCBI GI g115796
BLAST score 571
E value 1.0e-64
Match length 127
% identity 98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402560
Seq. ID LIB3431-054-P1-K1-D4
Method BLASTX
NCBI GI g3075488
BLAST score 518
E value 1.0e-52
Match length 117
% identity 85
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402561
Seq. ID LIB3431-054-P1-K1-D5
Method BLASTX
NCBI GI g3789948
BLAST score 709
E value 5.0e-75
Match length 149
% identity 91
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No. 402562
Seq. ID LIB3431-054-P1-K1-D7
Method BLASTX
NCBI GI g4239845
BLAST score 205
E value 6.0e-16
Match length 113
% identity 42
NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 402578
 Seq. ID LIB3431-054-P1-K1-G11
 Method BLASTX
 NCBI GI g3757521
 BLAST score 567
 E value 2.0e-58
 Match length 169
 % identity 58
 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 402579
 Seq. ID LIB3431-054-P1-K1-G3
 Method BLASTX
 NCBI GI g3789954
 BLAST score 550
 E value 1.0e-56
 Match length 122
 % identity 93
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 402580
 Seq. ID LIB3431-054-P1-K1-G4
 Method BLASTX
 NCBI GI g1707657
 BLAST score 538
 E value 5.0e-55
 Match length 167
 % identity 62
 NCBI Description (Z71640) DnaJ homologue [Pisum sativum]

Seq. No. 402581
 Seq. ID LIB3431-054-P1-K1-G5
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402582
 Seq. ID LIB3431-054-P1-K1-G7
 Method BLASTX
 NCBI GI g729478
 BLAST score 794
 E value 5.0e-85
 Match length 153
 % identity 98
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 402583
 Seq. ID LIB3431-054-P1-K1-H1
 Method BLASTX
 NCBI GI g3912968
 BLAST score 172
 E value 3.0e-12
 Match length 123
 % identity 30
 NCBI Description ALPHA-ADAPTIN HOMOLOG >gi_1890329_emb_CAA71991_ (Y11104)
 alpha-adaptin [Drosophila melanogaster]

Seq. No. 402584
 Seq. ID LIB3431-054-P1-K1-H11
 Method BLASTX
 NCBI GI g629670
 BLAST score 348
 E value 6.0e-33
 Match length 94
 % identity 68
 NCBI Description hypothetical protein - tomato

Seq. No. 402585
 Seq. ID LIB3431-054-P1-K1-H3
 Method BLASTX
 NCBI GI g3885894
 BLAST score 398
 E value 7.0e-39
 Match length 90
 % identity 87
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 402586
 Seq. ID LIB3431-054-P1-K1-H6
 Method BLASTX
 NCBI GI g22380
 BLAST score 512
 E value 6.0e-52
 Match length 127
 % identity 80
 NCBI Description (X59714) CAAT-box DNA binding protein subunit B (NF-YB)
 [Zea mays]

Seq. No. 402587
 Seq. ID LIB3431-054-P1-K1-H7
 Method BLASTX
 NCBI GI g320618
 BLAST score 335
 E value 3.0e-32
 Match length 88
 % identity 83
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 402588
 Seq. ID LIB3431-054-P1-K1-H9
 Method BLASTX
 NCBI GI g132105
 BLAST score 635
 E value 1.0e-66
 Match length 116
 % identity 100
 NCBI Description RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402589
 Seq. ID LIB3431-054-P1-N1-A10
 Method BLASTX
 NCBI GI g3913426
 BLAST score 300
 E value 2.0e-33
 Match length 118
 % identity 69
 NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532048_emb_CAA69074_ (Y07766) S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No. 402590
 Seq. ID LIB3431-054-P1-N1-A3
 Method BLASTX
 NCBI GI g1173347
 BLAST score 276
 E value 1.0e-48
 Match length 116
 % identity 77
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 402591
 Seq. ID LIB3431-054-P1-N1-A5
 Method BLASTX
 NCBI GI g6093830
 BLAST score 155
 E value 4.0e-10
 Match length 37
 % identity 81
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosystem II peptide [Spinacia oleracea]

Seq. No. 402607
 Seq. ID LIB3431-054-P1-N1-C2
 Method BLASTX
 NCBI GI g551047
 BLAST score 268
 E value 2.0e-23
 Match length 52
 % identity 96
 NCBI Description (X79277) type II LHCI [*Lolium temulentum*]

Seq. No. 402608
 Seq. ID LIB3431-054-P1-N1-C3
 Method BLASTX
 NCBI GI g417260
 BLAST score 288
 E value 1.0e-25
 Match length 127
 % identity 55
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [*Oryza sativa*]

Seq. No. 402609
 Seq. ID LIB3431-054-P1-N1-C4
 Method BLASTN
 NCBI GI g3885891
 BLAST score 241
 E value 1.0e-133
 Match length 245
 % identity 100
 NCBI Description *Oryza sativa* photosystem-1 F subunit precursor (PSI-F)
 mRNA, complete cds

Seq. No. 402610
 Seq. ID LIB3431-054-P1-N1-C5
 Method BLASTX
 NCBI GI g2832672
 BLAST score 587
 E value 1.0e-60
 Match length 135
 % identity 81
 NCBI Description (AL021712) nifU-like protein [*Arabidopsis thaliana*]

Seq. No. 402611
 Seq. ID LIB3431-054-P1-N1-C6
 Method BLASTX
 NCBI GI g131400
 BLAST score 284
 E value 1.0e-34
 Match length 130
 % identity 63
 NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
 >gi_81471_pir_S00409 photosystem II 10K protein precursor
 - spinach >gi_170127 (J03887) 10kd polypeptide precursor
 [*Spinacia oleracea*]

BLAST score 525
 E value 2.0e-53
 Match length 111
 % identity 91
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402618
 Seq. ID LIB3431-054-P1-N1-D5
 Method BLASTX
 NCBI GI g124226
 BLAST score 385
 E value 9.0e-59
 Match length 127
 % identity 92
 NCBI Description INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
 >gi_100278_pir_S21059 translation initiation factor
 eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104
 (X63542) eukaryotic initiation factor 5A (2) [Nicotiana
 plumbaginifolia]

Seq. No. 402619
 Seq. ID LIB3431-054-P1-N1-D8
 Method BLASTX
 NCBI GI g2191138
 BLAST score 241
 E value 1.0e-21
 Match length 92
 % identity 64
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis
 thaliana]

Seq. No. 402620
 Seq. ID LIB3431-054-P1-N1-E11
 Method BLASTX
 NCBI GI g6093830
 BLAST score 160
 E value 7.0e-11
 Match length 62
 % identity 31
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
 [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
 PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
 putative photosytem II peptide [Spinacia oleracea]

Seq. No. 402621
 Seq. ID LIB3431-054-P1-N1-E2
 Method BLASTN
 NCBI GI g3819352
 BLAST score 58
 E value 9.0e-24
 Match length 82
 % identity 93
 NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0813.rev

Seq. No. 402622
 Seq. ID LIB3431-054-P1-N1-E3
 Method BLASTX

Method BLASTX
 NCBI GI g2072555
 BLAST score 222
 E value 6.0e-18
 Match length 41
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402628
 Seq. ID LIB3431-054-P1-N1-F2
 Method BLASTX
 NCBI GI g132105
 BLAST score 396
 E value 1.0e-38
 Match length 74
 % identity 96
 NCBI Description RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402629
 Seq. ID LIB3431-054-P1-N1-F3
 Method BLASTX
 NCBI GI g115787
 BLAST score 332
 E value 6.0e-55
 Match length 115
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 402630
 Seq. ID LIB3431-054-P1-N1-F4
 Method BLASTX
 NCBI GI g606817
 BLAST score 182
 E value 3.0e-28
 Match length 69
 % identity 78
 NCBI Description (U08404) carbonic anhydrase [Oryza sativa]
 >gi_5917783_gb_AAD56038.1 AF182806_1 (AF182806) carbonic
 anhydrase 3 [Oryza sativa]

Seq. No. 402631
 Seq. ID LIB3431-054-P1-N1-F6
 Method BLASTX


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Seq. No.      402636
Seq. ID      LIB3431-054-P1-N1-G10
Method       BLASTX
NCBI GI      g2118307
BLAST score   166
E value      4.0e-24
Match length  91
% identity    55
NCBI Description cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
                >gi_804950_emb_CAA58893_(X84097) cysteine synthase
                [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac)
                thiol lyase [Arabidopsis thaliana]
```

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Seq. No.          402637
Seq. ID           LIB3431-054-P1-N1-G5
Method            BLASTX
NCBI GI           g2072555
BLAST score       230
E value           7.0e-19
Match length      44
% identity         98
NCBI Description   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
```

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Seq. No.          402638
Seq. ID           LIB3431-054-P1-N1-G6
Method            BLASTX
NCBI GI           g6015059
BLAST score       320
E value           9.0e-51
Match length      104
% identity         97
NCBI Description   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
                   (AF030517) translation elongation factor-1_alpha; EF-1
                   alpha [Oryza sativa]
```

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Seq. No.          402639
Seq. ID          LIB3431-054-P1-N1-G7
Method          BLASTX
NCBI GI         g729478
BLAST score      429
E value         1.0e-73
Match length     152
% identity       93
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                  >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
                  (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
                  a region of the predicted gene.; similar to
                  ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
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Seq. No.      402640
Seq. ID      LIB3431-054-P1-N1-H3
Method       BLASTX
NCBI GI      g3885894
BLAST score  253
```


Seq. No. 402645
 Seq. ID LIB3431-055-P1-N1-A1
 Method BLASTX
 NCBI GI g1644427
 BLAST score 248
 E value 3.0e-21
 Match length 59
 % identity 78
 NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 402646
 Seq. ID LIB3431-055-P1-N1-A11
 Method BLASTX
 NCBI GI g517500
 BLAST score 360
 E value 3.0e-34
 Match length 87
 % identity 80
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 402647
 Seq. ID LIB3431-055-P1-N1-A2
 Method BLASTX
 NCBI GI g131225
 BLAST score 216
 E value 2.0e-17
 Match length 56
 % identity 73
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402648
 Seq. ID LIB3431-055-P1-N1-A6
 Method BLASTX
 NCBI GI g693920
 BLAST score 414
 E value 2.0e-40
 Match length 80
 % identity 97
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No. 402649
 Seq. ID LIB3431-055-P1-N1-A7
 Method BLASTX
 NCBI GI g21699
 BLAST score 317
 E value 3.0e-29
 Match length 71
 % identity 83
 NCBI Description (X66013) cathepsin B [Triticum aestivum]

Seq. No. 402650

Match length 101
 % identity 85
 NCBI Description catalase (EC 1.11.1.6) catA - rice
 >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 402671
 Seq. ID LIB3431-055-P1-N1-E2
 Method BLASTN
 NCBI GI g3789951
 BLAST score 403
 E value 0.0e+00
 Match length 480
 % identity 96
 NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
 (Cab27) mRNA, nuclear gene encoding chloroplast protein,
 complete cds

Seq. No. 402672
 Seq. ID LIB3431-055-P1-N1-E3
 Method BLASTX
 NCBI GI g4507769
 BLAST score 257
 E value 7.0e-37
 Match length 98
 % identity 74
 NCBI Description ubiquitin-conjugating enzyme E2A (RAD6 homolog)
 >gi_1351346_sp_P49459_UBCA HUMAN UBIQUITIN-CONJUGATING
 ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN
 CARRIER PROTEIN) (HR6A) >gi_108016_pir_A41222
 ubiquitin-conjugating enzyme HHR6A - human >gi_184044
 (M74524) HHR6A (Human homologue of yeast RAD 6); putative
 [Homo sapiens]

Seq. No. 402673
 Seq. ID LIB3431-055-P1-N1-E9
 Method BLASTX
 NCBI GI g4335763
 BLAST score 333
 E value 6.0e-31
 Match length 122
 % identity 55
 NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 402674
 Seq. ID LIB3431-055-P1-N1-F10
 Method BLASTX
 NCBI GI g4337175
 BLAST score 168
 E value 5.0e-25
 Match length 114
 % identity 58
 NCBI Description (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
 gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
 gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
 gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 402675

09684016-101000

Seq. ID LIB3431-055-P1-N1-F2
 Method BLASTX
 NCBI GI g115787
 BLAST score 362
 E value 3.0e-50
 Match length 107
 % identity 98
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402676
 Seq. ID LIB3431-055-P1-N1-F3
 Method BLASTX
 NCBI GI g2407279
 BLAST score 211
 E value 2.0e-26
 Match length 66
 % identity 98
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 402677
 Seq. ID LIB3431-055-P1-N1-F5
 Method BLASTX
 NCBI GI g1321661
 BLAST score 427
 E value 5.0e-42
 Match length 83
 % identity 98
 NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 402678
 Seq. ID LIB3431-055-P1-N1-F6
 Method BLASTX
 NCBI GI g3036951
 BLAST score 343
 E value 2.0e-61
 Match length 122
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 402679
 Seq. ID LIB3431-055-P1-N1-F8
 Method BLASTN
 NCBI GI g2624325
 BLAST score 227
 E value 1.0e-124
 Match length 239
 % identity 99
 NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein (OsGRP1)

Seq. No. 402680
 Seq. ID LIB3431-055-P1-N1-F9

% identity 98
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402686
Seq. ID LIB3431-055-P1-N1-G5
Method BLASTX
NCBI GI g1617197
BLAST score 261
E value 2.0e-22
Match length 71
% identity 66

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 402687
Seq. ID LIB3431-055-P1-N1-G6
Method BLASTX
NCBI GI g131225
BLAST score 309
E value 3.0e-28
Match length 75
% identity 79

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402688
Seq. ID LIB3431-055-P1-N1-G8
Method BLASTX
NCBI GI g1076724
BLAST score 233
E value 1.0e-31
Match length 77
% identity 88

NCBI Description LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049 (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No. 402689
Seq. ID LIB3431-055-P1-N1-G9
Method BLASTX
NCBI GI g1617197
BLAST score 204
E value 7.0e-16
Match length 47
% identity 79

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 402690
Seq. ID LIB3431-055-P1-N1-H1
Method BLASTN
NCBI GI g3063523
BLAST score 117
E value 4.0e-59
Match length 281
% identity 86

NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 402691
Seq. ID LIB3431-055-P1-N1-H11
Method BLASTX
NCBI GI g3004565
BLAST score 255
E value 9.0e-22
Match length 94
% identity 55
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 402692
Seq. ID LIB3431-055-P1-N1-H2
Method BLASTN
NCBI GI g2773153
BLAST score 371
E value 0.0e+00
Match length 375
% identity 100
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No. 402693
Seq. ID LIB3431-055-P1-N1-H3
Method BLASTX
NCBI GI g548605
BLAST score 420
E value 4.0e-56
Match length 131
% identity 91
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 402694
Seq. ID LIB3431-055-P1-N1-H4
Method BLASTX
NCBI GI g115813
BLAST score 432
E value 1.0e-42
Match length 104
% identity 81
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402695
Seq. ID LIB3431-055-P1-N1-H5
Method BLASTX
NCBI GI g132105
BLAST score 521
E value 6.0e-53
Match length 99
% identity 97

E value 7.0e-34
 Match length 90
 % identity 90
 NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586
 (U85494) LON1 protease [Zea mays]

Seq. No. 402706
 Seq. ID LIB3431-055-P2-K1-C1
 Method BLASTX
 NCBI GI g3126854
 BLAST score 443
 E value 5.0e-44
 Match length 119
 % identity 84
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402707
 Seq. ID LIB3431-055-P2-K1-C11
 Method BLASTN
 NCBI GI g3885885
 BLAST score 32
 E value 3.0e-09
 Match length 32
 % identity 100
 NCBI Description Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
 complete cds

Seq. No. 402708
 Seq. ID LIB3431-055-P2-K1-C6
 Method BLASTN
 NCBI GI g303856
 BLAST score 139
 E value 4.0e-72
 Match length 227
 % identity 93
 NCBI Description Rice mRNA for ubiquitin protein fused to a ribosomal
 protein, complete cds

Seq. No. 402709
 Seq. ID LIB3431-055-P2-K1-C7
 Method BLASTX
 NCBI GI g517500
 BLAST score 160
 E value 1.0e-10
 Match length 61
 % identity 57
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
 protein [Zea mays] >gi_444338_prf__1906386A photosystem II
 OE17 protein [Pisum sativum]

Seq. No. 402710
 Seq. ID LIB3431-055-P2-K1-D11
 Method BLASTN
 NCBI GI g6016845
 BLAST score 66
 E value 1.0e-28
 Match length 108

Seq. ID LIB3431-055-P2-K1-F9
 Method BLASTX
 NCBI GI g2407281
 BLAST score 645
 E value 1.0e-67
 Match length 122
 % identity 97
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 402717
 Seq. ID LIB3431-055-P2-K1-G10
 Method BLASTN
 NCBI GI g3075487
 BLAST score 99
 E value 1.0e-48
 Match length 123
 % identity 95
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 402718
 Seq. ID LIB3431-055-P2-K1-G2
 Method BLASTN
 NCBI GI g20262
 BLAST score 227
 E value 1.0e-125
 Match length 231
 % identity 100
 NCBI Description O.sativa light-induced mRNA

Seq. No. 402719
 Seq. ID LIB3431-055-P2-K1-H11
 Method BLASTX
 NCBI GI g3004565
 BLAST score 340
 E value 4.0e-32
 Match length 97
 % identity 66
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 402720
 Seq. ID LIB3431-055-P2-K1-H12
 Method BLASTX
 NCBI GI g4678920
 BLAST score 227
 E value 1.0e-18
 Match length 102
 % identity 48
 NCBI Description (AL049711) putative heat shock transcription factor [Arabidopsis thaliana]

Seq. No. 402721
 Seq. ID LIB3431-055-P2-K1-H2
 Method BLASTN
 NCBI GI g2773153
 BLAST score 171

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402727
 Seq. ID LIB3431-056-P1-K1-A11
 Method BLASTX
 NCBI GI g1519251
 BLAST score 673
 E value 7.0e-71
 Match length 150
 % identity 91
 NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 402728
 Seq. ID LIB3431-056-P1-K1-A2
 Method BLASTX
 NCBI GI g3126854
 BLAST score 488
 E value 3.0e-49
 Match length 114
 % identity 85
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402729
 Seq. ID LIB3431-056-P1-K1-A3
 Method BLASTN
 NCBI GI g4959460
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 402730
 Seq. ID LIB3431-056-P1-K1-A4
 Method BLASTN
 NCBI GI g4959460
 BLAST score 35
 E value 6.0e-10
 Match length 35
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 402731
 Seq. ID LIB3431-056-P1-K1-A5
 Method BLASTX
 NCBI GI g5734634
 BLAST score 318
 E value 3.0e-29
 Match length 107
 % identity 53

NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No. 402732
Seq. ID LIB3431-056-P1-K1-A6
Method BLASTX
NCBI GI g3288821
BLAST score 259
E value 2.0e-47
Match length 110
% identity 87

NCBI Description (AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]
>gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 402733
Seq. ID LIB3431-056-P1-K1-A8
Method BLASTN
NCBI GI g1245938
BLAST score 35
E value 5.0e-10
Match length 35
% identity 100

NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No. 402734
Seq. ID LIB3431-056-P1-K1-B1
Method BLASTX
NCBI GI g132096
BLAST score 500
E value 8.0e-60
Match length 125
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR (RUBISCO SMALL SUBUNIT A) >gi_68095_pir_RKRZS6
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_ (D00644) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa]

Seq. No. 402735
Seq. ID LIB3431-056-P1-K1-B10
Method BLASTX
NCBI GI g4678311
BLAST score 272
E value 6.0e-24
Match length 77
% identity 68

NCBI Description (AL049655) aquaporin/MIP-like protein [Arabidopsis thaliana]

Seq. No. 402736
Seq. ID LIB3431-056-P1-K1-B11
Method BLASTX
NCBI GI g1076724

BLAST score 451
E value 4.0e-66
Match length 141
% identity 87
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 402737
Seq. ID LIB3431-056-P1-K1-B12
Method BLASTX
NCBI GI g3789952
BLAST score 652
E value 2.0e-68
Match length 132
% identity 96
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]

Seq. No. 402738
Seq. ID LIB3431-056-P1-K1-B2
Method BLASTN
NCBI GI g433216
BLAST score 115
E value 6.0e-58
Match length 118
% identity 99
NCBI Description Rice mRNA for ascorbate peroxidase (gene name SS622),
partial cds

Seq. No. 402739
Seq. ID LIB3431-056-P1-K1-B4
Method BLASTX
NCBI GI g1173347
BLAST score 326
E value 2.0e-39
Match length 103
% identity 87
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
>gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
(X65540) sedoheptulose-1,7-bisphosphatase [Triticum
aestivum]

Seq. No. 402740
Seq. ID LIB3431-056-P1-K1-B6
Method BLASTX
NCBI GI g2407281
BLAST score 673
E value 6.0e-71
Match length 133
% identity 94
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]

Seq. No. 402741

Seq. ID LIB3431-056-P1-K1-B7
 Method BLASTX
 NCBI GI g2072555
 BLAST score 193
 E value 1.0e-14
 Match length 35
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402742
 Seq. ID LIB3431-056-P1-K1-B8
 Method BLASTX
 NCBI GI g4585882
 BLAST score 469
 E value 7.0e-51
 Match length 145
 % identity 66
 NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
 [Arabidopsis thaliana]

Seq. No. 402743
 Seq. ID LIB3431-056-P1-K1-B9
 Method BLASTX
 NCBI GI g2264373
 BLAST score 355
 E value 9.0e-34
 Match length 103
 % identity 63
 NCBI Description (AC002354) putative NAM/no apical meristem protein
 [Arabidopsis thaliana]

Seq. No. 402744
 Seq. ID LIB3431-056-P1-K1-C1
 Method BLASTX
 NCBI GI g4079798
 BLAST score 231
 E value 6.0e-30
 Match length 93
 % identity 78
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza
 sativa]

Seq. No. 402745
 Seq. ID LIB3431-056-P1-K1-C10
 Method BLASTX
 NCBI GI g3885896
 BLAST score 524
 E value 2.0e-53
 Match length 100
 % identity 100
 NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 402746
 Seq. ID LIB3431-056-P1-K1-C12
 Method BLASTX

NCBI GI g132105
 BLAST score 537
 E value 6.0e-55
 Match length 111
 % identity 91
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402747
 Seq. ID LIB3431-056-P1-K1-C2
 Method BLASTX
 NCBI GI g2073375
 BLAST score 459
 E value 2.0e-54
 Match length 110
 % identity 90
 NCBI Description (D85317) farnesyl pyrophosphate synthase [Oryza sativa] >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate synthase [Oryza sativa]

Seq. No. 402748
 Seq. ID LIB3431-056-P1-K1-C3
 Method BLASTX
 NCBI GI g417260
 BLAST score 421
 E value 3.0e-41
 Match length 128
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No. 402749
 Seq. ID LIB3431-056-P1-K1-C4
 Method BLASTX
 NCBI GI g2407281
 BLAST score 650
 E value 3.0e-68
 Match length 125
 % identity 94
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 402750
 Seq. ID LIB3431-056-P1-K1-C5
 Method BLASTX
 NCBI GI g2191151
 BLAST score 170
 E value 4.0e-17
 Match length 87

% identity 60
 NCBI Description (AF007269) contains similarity to membrane associated salt-inducible protein [Arabidopsis thaliana]

Seq. No. 402751
 Seq. ID LIB3431-056-P1-K1-C6
 Method BLASTX
 NCBI GI g548605
 BLAST score 541
 E value 2.0e-55
 Match length 118
 % identity 91
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 402752
 Seq. ID LIB3431-056-P1-K1-C7
 Method BLASTX
 NCBI GI g871931
 BLAST score 416
 E value 1.0e-40
 Match length 108
 % identity 78
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 402753
 Seq. ID LIB3431-056-P1-K1-C9
 Method BLASTX
 NCBI GI g2688828
 BLAST score 169
 E value 7.0e-12
 Match length 82
 % identity 43
 NCBI Description (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No. 402754
 Seq. ID LIB3431-056-P1-K1-D1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402755
 Seq. ID LIB3431-056-P1-K1-D12
 Method BLASTX
 NCBI GI g671740
 BLAST score 606
 E value 5.0e-63

Match length 111
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402756
 Seq. ID LIB3431-056-P1-K1-D3
 Method BLASTX
 NCBI GI g1076660
 BLAST score 219
 E value 9.0e-20
 Match length 126
 % identity 45
 NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 402757
 Seq. ID LIB3431-056-P1-K1-D4
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 9.0e-11
 Match length 36
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402758
 Seq. ID LIB3431-056-P1-K1-D5
 Method BLASTN
 NCBI GI g218209
 BLAST score 135
 E value 9.0e-70
 Match length 246
 % identity 93
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 402759
 Seq. ID LIB3431-056-P1-K1-D6
 Method BLASTX
 NCBI GI g3738261
 BLAST score 209
 E value 9.0e-17
 Match length 48
 % identity 92
 NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No. 402760
 Seq. ID LIB3431-056-P1-K1-D7
 Method BLASTX
 NCBI GI g320618
 BLAST score 648
 E value 6.0e-68


```
BLAST score      235
E value         2.0e-19
Match length    44
% identity      100
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]
```

```
Seq. No.          402771
Seq. ID           LIB3431-056-P1-K1-F1
Method            BLASTX
NCBI GI           g115787
BLAST score       636
E value           2.0e-74
Match length      142
% identity        95
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      402772
Seq. ID      LIB3431-056-P1-K1-F10
Method       BLASTX
NCBI GI      g1173347
BLAST score   605
E value      4.0e-63
Match length  117
% identity    95
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
                3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                aestivum]
```

```
Seq. No.          402773
Seq. ID           LIB3431-056-P1-K1-F12
Method            BLASTX
NCBI GI           g3913808
BLAST score       477
E value           6.0e-48
Match length      102
% identity        88
NCBI Description  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
                  SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120)
                  ferrochelatase [Oryza sativa]
```

```
Seq. No.          402774
Seq. ID           LIB3431-056-P1-K1-F2
Method            BLASTX
NCBI GI           g585350
BLAST score       384
E value           3.0e-37
Match length      109
% identity        68
NCBI Description   CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
```

```
>gi_419753_pir_S31099 casein kinase II (EC 2.7.1.-)
alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
>gi_391605_dbj_BAA01091_1 (D10247) casein kinase II
catalytic subunit [Arabidopsis thaliana]
```

```
Seq. No.          402775
Seq. ID           LIB3431-056-P1-K1-F3
Method            BLASTX
NCBI GI           g115787
BLAST score       529
E value           4.0e-54
Match length      121
% identity        88
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      402777
Seq. ID      LIB3431-056-P1-K1-F6
Method       BLASTX
NCBI GI      g5689238
BLAST score   341
E value      2.0e-32
Match length  73
% identity    86
NCBI Description (AB024292) histidine-containing phosphotransfer protein
                [Zea mays]
```

```
Seq. No.      402779
Seq. ID       LIB3431-056-P1-K1-F9
Method        BLASTX
NCBI GI       q4836892
```

BLAST score 430
 E value 2.0e-42
 Match length 138
 % identity 58
 NCBI Description (AC007369) Putative RNA helicase [Arabidopsis thaliana]

Seq. No. 402780
 Seq. ID LIB3431-056-P1-K1-G1
 Method BLASTX
 NCBI GI g3335349
 BLAST score 416
 E value 1.0e-40
 Match length 155
 % identity 54
 NCBI Description (AC004512) Similar to gb_U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb_T42908, gb_AA586170 and gb_AA395125 come from this gene. [Arabidopsis thaliana]

Seq. No. 402781
 Seq. ID LIB3431-056-P1-K1-G10
 Method BLASTX
 NCBI GI g5326825
 BLAST score 164
 E value 3.0e-11
 Match length 90
 % identity 32
 NCBI Description (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]

Seq. No. 402782
 Seq. ID LIB3431-056-P1-K1-G12
 Method BLASTX
 NCBI GI g320618
 BLAST score 512
 E value 4.0e-52
 Match length 114
 % identity 85
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 402783
 Seq. ID LIB3431-056-P1-K1-G2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402784

```
Seq. ID      LIB3431-056-P1-K1-G3
Method       BLASTX
NCBI GI      g320618
BLAST score   532
E value      2.0e-54
Match length  117
% identity    86
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]
```

```
Seq. No.          402785
Seq. ID           LIB3431-056-P1-K1-G4
Method            BLASTX
NCBI GI           g320618
BLAST score       292
E value           2.0e-26
Match length      73
% identity        74
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
```

```
Seq. No.          402786
Seq. ID           LIB3431-056-P1-K1-G5
Method            BLASTX
NCBI GI           g548605
BLAST score       588
E value           7.0e-61
Match length      130
% identity        90
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

```
Seq. No.      402787
Seq. ID      LIB3431-056-P1-K1-G6
Method       BLASTX
NCBI GI      g417154
BLAST score   526
E value      7.0e-54
Match length  105
% identity    97
NCBI Description  HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock
protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
(HSP82) [Oryza sativa]
```

Seq. No.	402788
Seq. ID	LIB3431-056-P1-K1-G7
Method	BLASTN

NCBI GI g1261857
 BLAST score 54
 E value 2.0e-21
 Match length 54
 % identity 100
 NCBI Description Rice CatA gene for catalase, complete cds

Seq. No. 402789
 Seq. ID LIB3431-056-P1-K1-G8
 Method BLASTX
 NCBI GI g4678338
 BLAST score 202
 E value 1.0e-15
 Match length 48
 % identity 73
 NCBI Description (AL049658) putative protein [Arabidopsis thaliana]

Seq. No. 402790
 Seq. ID LIB3431-056-P1-K1-H1
 Method BLASTN
 NCBI GI g3345476
 BLAST score 132
 E value 7.0e-68
 Match length 241
 % identity 96
 NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 402791
 Seq. ID LIB3431-056-P1-K1-H10
 Method BLASTN
 NCBI GI g2570512
 BLAST score 112
 E value 3.0e-56
 Match length 212
 % identity 100
 NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 402792
 Seq. ID LIB3431-056-P1-K1-H12
 Method BLASTN
 NCBI GI g20191
 BLAST score 279
 E value 1.0e-156
 Match length 279
 % identity 100
 NCBI Description O.sativa mRNA for catalase

Seq. No. 402793
 Seq. ID LIB3431-056-P1-K1-H2
 Method BLASTX
 NCBI GI g133867
 BLAST score 558
 E value 2.0e-57
 Match length 124
 % identity 85
 NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal

09684016 101000

```
Seq. No.      402800
Seq. ID      LIB3431-056-P1-N1-A11
Method       BLASTN
NCBI GI      g2331130
BLAST score   100
E value      8.0e-49
Match length 148
% identity   92
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds
```

```
Seq. No.      402802
Seq. ID       LIB3431-056-P1-N1-A2
Method        BLASTX
NCBI GI       g3126854
BLAST score    349
E value       9.0e-33
Match length   66
% identity     100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

51764

Seq. No. 402813
 Seq. ID LIB3431-056-P1-N1-C1
 Method BLASTX
 NCBI GI g4079798
 BLAST score 414
 E value 2.0e-40
 Match length 81
 % identity 99
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 402814
 Seq. ID LIB3431-056-P1-N1-C10
 Method BLASTX
 NCBI GI g3885896
 BLAST score 524
 E value 2.0e-53
 Match length 100
 % identity 100
 NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 402815
 Seq. ID LIB3431-056-P1-N1-C12
 Method BLASTN
 NCBI GI g218209
 BLAST score 37
 E value 3.0e-11
 Match length 53
 % identity 92
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 402816
 Seq. ID LIB3431-056-P1-N1-C2
 Method BLASTX
 NCBI GI g2073375
 BLAST score 576
 E value 2.0e-59
 Match length 107
 % identity 100
 NCBI Description (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
 >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate synthase [Oryza sativa]

Seq. No. 402817
 Seq. ID LIB3431-056-P1-N1-C3
 Method BLASTX
 NCBI GI g417260
 BLAST score 321
 E value 1.0e-29
 Match length 106
 % identity 61
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402818
 Seq. ID LIB3431-056-P1-N1-C4
 Method BLASTX
 NCBI GI g671740
 BLAST score 361
 E value 3.0e-34
 Match length 70
 % identity 97
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402819
 Seq. ID LIB3431-056-P1-N1-C6
 Method BLASTX
 NCBI GI g548605
 BLAST score 599
 E value 5.0e-62
 Match length 131
 % identity 91
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 402820
 Seq. ID LIB3431-056-P1-N1-C7
 Method BLASTX
 NCBI GI g871931
 BLAST score 161
 E value 5.0e-11
 Match length 44
 % identity 75
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 402821
 Seq. ID LIB3431-056-P1-N1-D1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 228
 E value 1.0e-18
 Match length 42
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402822
 Seq. ID LIB3431-056-P1-N1-D12
 Method BLASTX
 NCBI GI g671740
 BLAST score 433
 E value 1.0e-42
 Match length 78
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402823
 Seq. ID LIB3431-056-P1-N1-D3
 Method BLASTX
 NCBI GI g1076660
 BLAST score 222
 E value 6.0e-18
 Match length 89
 % identity 57
 NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122
 (S74753) MybSt1=Myb-related transcriptional activator
 {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
 leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 402824
 Seq. ID LIB3431-056-P1-N1-D5
 Method BLASTN
 NCBI GI g218209
 BLAST score 39
 E value 2.0e-12
 Match length 55
 % identity 93
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 POSSS2106

Seq. No. 402825
 Seq. ID LIB3431-056-P1-N1-D7
 Method BLASTX
 NCBI GI g115787
 BLAST score 409
 E value 6.0e-40
 Match length 77
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 402826
 Seq. ID LIB3431-056-P1-N1-D8
 Method BLASTX
 NCBI GI g3885892
 BLAST score 544
 E value 9.0e-56
 Match length 102
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402827
 Seq. ID LIB3431-056-P1-N1-D9
 Method BLASTX
 NCBI GI g3885892
 BLAST score 286
 E value 2.0e-25
 Match length 57

% identity 100
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402828
Seq. ID LIB3431-056-P1-N1-E1
Method BLASTX
NCBI GI g3789954
BLAST score 611
E value 2.0e-63
Match length 113
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 402829
Seq. ID LIB3431-056-P1-N1-E11
Method BLASTX
NCBI GI g1076724
BLAST score 374
E value 8.0e-36
Match length 72
% identity 94
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 402830
Seq. ID LIB3431-056-P1-N1-E12
Method BLASTX
NCBI GI g1084461
BLAST score 287
E value 1.0e-25
Match length 98
% identity 60
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 402831
Seq. ID LIB3431-056-P1-N1-E2
Method BLASTX
NCBI GI g115813
BLAST score 234
E value 2.0e-19
Match length 56
% identity 80
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402832
Seq. ID LIB3431-056-P1-N1-E7
Method BLASTX
NCBI GI g5733872
BLAST score 182
E value 2.0e-13
Match length 57
% identity 60
NCBI Description (AC007932) Similar to gi_4982048 ribosomal protein L18 from

Seq. No. 402837
 Seq. ID LIB3431-056-P1-N1-F11
 Method BLASTX
 NCBI GI g2244734
 BLAST score 166
 E value 2.0e-11
 Match length 32
 % identity 97
 NCBI Description (D88414) actin [*Gossypium hirsutum*]

Seq. No. 402838
 Seq. ID LIB3431-056-P1-N1-F2
 Method BLASTX
 NCBI GI g585350
 BLAST score 496
 E value 5.0e-50
 Match length 110
 % identity 83
 NCBI Description CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
 >gi_419753_pir_S31099 casein kinase II (EC 2.7.1.-)
 alpha-type chain (clone ATCKA2) - *Arabidopsis thaliana*
 >gi_391605_dbj_BAA01091 (D10247) casein kinase II
 catalytic subunit [*Arabidopsis thaliana*]

Seq. No. 402839
 Seq. ID LIB3431-056-P1-N1-F3
 Method BLASTX
 NCBI GI g3036951
 BLAST score 427
 E value 6.0e-42
 Match length 80
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [*Nicotiana sylvestris*]

Seq. No. 402840
 Seq. ID LIB3431-056-P1-N1-F5
 Method BLASTN
 NCBI GI g1619603
 BLAST score 370
 E value 0.0e+00
 Match length 414
 % identity 97
 NCBI Description O.sativa mRNA for lipid transfer protein
 >gi_1667589_gb_U77295_OSU77295 *Oryza sativa* lipid transfer
 protein (LTP) mRNA, complete cds

Seq. No. 402841
 Seq. ID LIB3431-056-P1-N1-F9
 Method BLASTX
 NCBI GI g2673917
 BLAST score 305
 E value 1.0e-27
 Match length 80
 % identity 66
 NCBI Description (AC002561) putative ATP-dependent RNA helicase [*Arabidopsis*]

069416-10000

```
Seq. No.          402846
Seq. ID           LIB3431-056-P1-N1-G2
Method            BLASTX
NCBI GI           g2072555
BLAST score       228
E value           1.0e-18
Match length      42
% identity        100
```

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 402847
Seq. ID LIB3431-056-P1-N1-G3
Method BLASTX
NCBI GI g115787
BLAST score 676
E value 4.0e-71
Match length 130
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 402848
Seq. ID LIB3431-056-P1-N1-G4
Method BLASTX
NCBI GI g3036951
BLAST score 650
E value 4.0e-68
Match length 124
% identity 98

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
[Nicotiana sylvestris]

Seq. No. 402849
Seq. ID LIB3431-056-P1-N1-G5
Method BLASTX
NCBI GI g548605
BLAST score 301
E value 2.0e-27
Match length 64
% identity 92

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[Hordeum vulgare]

Seq. No. 402850
Seq. ID LIB3431-056-P1-N1-G6
Method BLASTX
NCBI GI g417154
BLAST score 392
E value 7.0e-38
Match length 93
% identity 85

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock
protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
(HSP82) [Oryza sativa]

Seq. No. 402851

Seq. ID LIB3431-056-P1-N1-G9
Method BLASTX
NCBI GI g4006881
BLAST score 585
E value 2.0e-60
Match length 139
% identity 79
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 402852
Seq. ID LIB3431-056-P1-N1-H1
Method BLASTN
NCBI GI g3345476
BLAST score 342
E value 0.0e+00
Match length 386
% identity 97
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 402853
Seq. ID LIB3431-056-P1-N1-H2
Method BLASTN
NCBI GI g22469
BLAST score 34
E value 1.0e-09
Match length 38
% identity 97
NCBI Description Maize mRNA for cytoplasmic ribosomal protein S11

Seq. No. 402854
Seq. ID LIB3431-056-P1-N1-H5
Method BLASTN
NCBI GI g14264
BLAST score 67
E value 3.0e-29
Match length 115
% identity 90
NCBI Description T.aestivum gene for sedoheptulose-1,7-bisphosphatase

Seq. No. 402855
Seq. ID LIB3431-056-P1-N1-H9
Method BLASTX
NCBI GI g671740
BLAST score 546
E value 6.0e-56
Match length 99
% identity 100
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402856
Seq. ID LIB3431-058-P1-K1-A1
Method BLASTX
NCBI GI g3355468
BLAST score 355
E value 1.0e-33
Match length 96

% identity 85
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 402857
 Seq. ID LIB3431-058-P1-K1-A10
 Method BLASTX
 NCBI GI g2244749
 BLAST score 383
 E value 7.0e-37
 Match length 112
 % identity 66
 NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 402858
 Seq. ID LIB3431-058-P1-K1-A12
 Method BLASTX
 NCBI GI g3345477
 BLAST score 214
 E value 4.0e-17
 Match length 41
 % identity 95
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402859
 Seq. ID LIB3431-058-P1-K1-A2
 Method BLASTX
 NCBI GI g1514643
 BLAST score 180
 E value 4.0e-26
 Match length 102
 % identity 63
 NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 402860
 Seq. ID LIB3431-058-P1-K1-A3
 Method BLASTN
 NCBI GI g1159878
 BLAST score 52
 E value 3.0e-20
 Match length 64
 % identity 95
 NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)

Seq. No. 402861
 Seq. ID LIB3431-058-P1-K1-A4
 Method BLASTX
 NCBI GI g2072555
 BLAST score 165
 E value 3.0e-11
 Match length 32
 % identity 94
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402862

```
Seq. ID      LIB3431-058-P1-K1-A5
Method       BLASTX
NCBI GI      g2462760
BLAST score  143
E value      8.0e-09
Match length 75
% identity   39
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.          402863
Seq. ID           LIB3431-058-P1-K1-A6
Method            BLASTX
NCBI GI           g3402713
BLAST score       379
E value           2.0e-36
Match length      123
% identity        60
NCBI Description   (AC004261) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      402864
Seq. ID      LIB3431-058-P1-K1-A7
Method       BLASTX
NCBI GI      g132105
BLAST score   494
E value      6.0e-50
Match length  109
% identity    83
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

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Seq. No.      402865
Seq. ID       LIB3431-058-P1-K1-A8
Method        BLASTX
NCBI GI       g3046693
BLAST score    573
E value       3.0e-59
Match length   136
% identity     74
NCBI Description (AL022140) receptor like protein (fragment) [Arabidopsis thaliana]
```

Seq. No.	402866
Seq. ID	LIB3431-058-P1-K1-A9
Method	BLASTX
NCBI GI	g3550983
BLAST score	358
E value	5.0e-34
Match length	98
% identity	68
NCBI Description	(AB010690) mutM homologue-2 [Arabidopsis thaliana]

>gi_3820622 (AF099971) putative formamidopyrimidine-DNA glycosylase 2 [Arabidopsis thaliana]
 >gi_5903054_gb_AAD55613.1_AC008016_23 (AC008016) Identical to gb_AB010690 mutM homologue-2 (formamidopyrimidine-DNA glycosylase 1) from Arabidopsis thaliana. EST gb_Z18192 comes from this gene

Seq. No. 402867
 Seq. ID LIB3431-058-P1-K1-B10
 Method BLASTX
 NCBI GI g3885886
 BLAST score 748
 E value 1.0e-79
 Match length 144
 % identity 100
 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402868
 Seq. ID LIB3431-058-P1-K1-B11
 Method BLASTX
 NCBI GI g2582381
 BLAST score 458
 E value 4.0e-46
 Match length 87
 % identity 93
 NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No. 402869
 Seq. ID LIB3431-058-P1-K1-B12
 Method BLASTX
 NCBI GI g2570511
 BLAST score 485
 E value 5.0e-49
 Match length 92
 % identity 99
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 402870
 Seq. ID LIB3431-058-P1-K1-B2
 Method BLASTX
 NCBI GI g3850566
 BLAST score 236
 E value 1.0e-22
 Match length 156
 % identity 40
 NCBI Description (AC005278) F15K9.3 [Arabidopsis thaliana]

Seq. No. 402871
 Seq. ID LIB3431-058-P1-K1-B3
 Method BLASTN
 NCBI GI g5730046
 BLAST score 35
 E value 3.0e-10
 Match length 35
 % identity 100
 NCBI Description Homo sapiens solute carrier family 17 (sodium phosphate),

member 3 (SLC17A3) mRNA >gi_2062691_gb U90545 HSU90545
Human sodium phosphate transporter (NPT4) mRNA, complete
cds

Seq. No. 402872
Seq. ID LIB3431-058-P1-K1-B5
Method BLASTX
NCBI GI g430947
BLAST score 360
E value 3.0e-34
Match length 102
% identity 71
NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein
[Arabidopsis thaliana]

Seq. No. 402873
Seq. ID LIB3431-058-P1-K1-B6
Method BLASTX
NCBI GI g132105
BLAST score 468
E value 4.0e-52
Match length 101
% identity 100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 402874
Seq. ID LIB3431-058-P1-K1-B7
Method BLASTX
NCBI GI g21839
BLAST score 734
E value 5.0e-78
Match length 148
% identity 93
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402875
Seq. ID LIB3431-058-P1-K1-B8
Method BLASTX
NCBI GI g82080
BLAST score 152
E value 4.0e-10
Match length 68
% identity 51
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 402876
Seq. ID LIB3431-058-P1-K1-B9

Seq. No. 402887
 Seq. ID LIB3431-058-P1-K1-C9
 Method BLASTX
 NCBI GI g5816996
 BLAST score 325
 E value 4.0e-30
 Match length 88
 % identity 73
 NCBI Description (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No. 402888
 Seq. ID LIB3431-058-P1-K1-D1
 Method BLASTX
 NCBI GI g4587563
 BLAST score 301
 E value 2.0e-27
 Match length 81
 % identity 77
 NCBI Description (AC006550) Similar to gb_U51990 pre-mRNA-splicing factor hPrp18 from Homo sapiens. ESTs gb_T46391 and gb_AA721815 come from this gene. [Arabidopsis thaliana]

Seq. No. 402889
 Seq. ID LIB3431-058-P1-K1-D10
 Method BLASTN
 NCBI GI g6015437
 BLAST score 38
 E value 7.0e-12
 Match length 50
 % identity 67
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402890
 Seq. ID LIB3431-058-P1-K1-D11
 Method BLASTX
 NCBI GI g115796
 BLAST score 482
 E value 4.0e-55
 Match length 112
 % identity 96
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402891
 Seq. ID LIB3431-058-P1-K1-D12
 Method BLASTX
 NCBI GI g6016151
 BLAST score 492
 E value 9.0e-50
 Match length 128
 % identity 77
 NCBI Description IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT SHOCK PROTEIN 70 HOMOLOG 3) >gi_1575130 (U58209) luminal

09684016 101000

```
Seq. No.          402893
Seq. ID           LIB3431-058-P1-K1-D3
Method            BLASTN
NCBI GI           g4097337
BLAST score       304
E value           1.0e-170
Match length      368
% identity        99
NCBI Description   Oryza sativa metallothionein-like protein mRNA, complete
                  cds
```

[illegible]

```
Seq. No.      402895
Seq. ID      LIB3431-058-P1-K1-D6
Method       BLASTX
NCBI GI      g1835731
BLAST score   564
E value      3.0e-58
Match length  110
% identity    99
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

```
Seq. No.      402896
Seq. ID      LIB3431-058-P1-K1-D7
Method       BLASTX
NCBI GI      g2130043
BLAST score   600
E value      3.0e-62
Match length  145
% identity    82
NCBI Description  Mg-chelatase chain Xantha-h - barley (fragment) >gi 847873.2
```

0964016 30000

Seq. No.	402901
Seq. ID	LIB3431-058-P1-K1-E4
Method	BLASTX
NCBI GI	g132105
BLAST score	479
E value	3.0e-48
Match length	109

% identity 85
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402902
 Seq. ID LIB3431-058-P1-K1-E5
 Method BLASTX
 NCBI GI g132105
 BLAST score 372
 E value 8.0e-36
 Match length 90
 % identity 82

NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402903
 Seq. ID LIB3431-058-P1-K1-E7
 Method BLASTX
 NCBI GI g2570511
 BLAST score 244
 E value 7.0e-21
 Match length 86
 % identity 57

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 402904
 Seq. ID LIB3431-058-P1-K1-E8
 Method BLASTX
 NCBI GI g132105
 BLAST score 396
 E value 2.0e-59
 Match length 133
 % identity 86

NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

```
Seq. No.      402905
Seq. ID      LIB3431-058-P1-K1-E9
Method       BLASTX
NCBI GI      g2245020
BLAST score   212
E value      7.0e-17
Match length  137
% identity   40
NCBI Description (Z97341) growth regulator like protein [Arabidopsis
thaliana]
```

```
Seq. No.          402906
Seq. ID           LIB3431-058-P1-K1-F12
Method            BLASTX
NCBI GI           g3885894
BLAST score       447
E value           2.0e-44
Match length      101
% identity        87
NCBI Description  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
```

```
Seq. No.          402907
Seq. ID           LIB3431-058-P1-K1-F2
Method            BLASTX
NCBI GI           g2501189
BLAST score       313
E value           3.0e-43
Match length      107
% identity        88
NCBI Description   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
```

```
Seq. No.      402908
Seq. ID      LIB3431-058-P1-K1-F4
Method       BLASTX
NCBI GI      g2924520
BLAST score   486
E value      6.0e-49
Match length  151
% identity    63
NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)
               [Arabidopsis thaliana]
```

Seq. No.	402909
Seq. ID	LIB3431-058-P1-K1-F8
Method	BLASTX
NCBI GI	g3126854
BLAST score	713
E value	1.0e-75
Match length	133
% identity	98
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	402910
Seq. ID	LIB3431-058-P1-K1-F9

Method BLASTN
 NCBI GI g3821780
 BLAST score 34
 E value 2.0e-09
 Match length 34
 % identity 100
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 402911
 Seq. ID LIB3431-058-P1-K1-G1
 Method BLASTN
 NCBI GI g20262
 BLAST score 300
 E value 1.0e-168
 Match length 328
 % identity 98
 NCBI Description O.sativa light-induced mRNA

Seq. No. 402912
 Seq. ID LIB3431-058-P1-K1-G10
 Method BLASTX
 NCBI GI g4581207
 BLAST score 570
 E value 6.0e-61
 Match length 145
 % identity 81
 NCBI Description (Y17914) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No. 402913
 Seq. ID LIB3431-058-P1-K1-G12
 Method BLASTX
 NCBI GI g417260
 BLAST score 416
 E value 1.0e-40
 Match length 127
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402914
 Seq. ID LIB3431-058-P1-K1-G3
 Method BLASTX
 NCBI GI g4538934
 BLAST score 275
 E value 4.0e-24
 Match length 102
 % identity 53
 NCBI Description (AL049483) putative leucine-rich-repeat protein
 [Arabidopsis thaliana]

Seq. No. 402915
 Seq. ID LIB3431-058-P1-K1-G4
 Method BLASTN
 NCBI GI g3885891
 BLAST score 118

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402920
 Seq. ID LIB3431-058-P1-K1-H12
 Method BLASTX
 NCBI GI g5916444
 BLAST score 240
 E value 4.0e-20
 Match length 120
 % identity 40
 NCBI Description (AC007633) putative protein [Arabidopsis thaliana]

Seq. No. 402921
 Seq. ID LIB3431-058-P1-K1-H2
 Method BLASTX
 NCBI GI g3789954
 BLAST score 607
 E value 3.0e-63
 Match length 120
 % identity 95
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 402922
 Seq. ID LIB3431-058-P1-K1-H6
 Method BLASTX
 NCBI GI g4585882
 BLAST score 446
 E value 2.0e-44
 Match length 117
 % identity 74
 NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
 [Arabidopsis thaliana]

Seq. No. 402923
 Seq. ID LIB3431-058-P1-K1-H8
 Method BLASTX
 NCBI GI g132105
 BLAST score 455
 E value 2.0e-45
 Match length 106
 % identity 84
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402924
 Seq. ID LIB3431-058-P1-K1-H9

Method BLASTX
 NCBI GI g3913018
 BLAST score 585
 E value 1.0e-60
 Match length 118
 % identity 100
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 402925
 Seq. ID LIB3431-058-P1-N1-A1
 Method BLASTX
 NCBI GI g3355468
 BLAST score 324
 E value 2.0e-38
 Match length 106
 % identity 85
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 402926
 Seq. ID LIB3431-058-P1-N1-A10
 Method BLASTX
 NCBI GI g2274988
 BLAST score 281
 E value 8.0e-25
 Match length 96
 % identity 55
 NCBI Description (AJ000226) partial sequence, homology to serine hydroxymethyltransferases [Hordeum vulgare]

Seq. No. 402927
 Seq. ID LIB3431-058-P1-N1-A11
 Method BLASTX
 NCBI GI g517500
 BLAST score 311
 E value 1.0e-28
 Match length 77
 % identity 81
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 402928
 Seq. ID LIB3431-058-P1-N1-A12
 Method BLASTX
 NCBI GI g3345477
 BLAST score 216
 E value 2.0e-17
 Match length 40
 % identity 100
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402929
 Seq. ID LIB3431-058-P1-N1-A2
 Method BLASTX

NCBI GI g1514643
 BLAST score 168
 E value 3.0e-26
 Match length 144
 % identity 45
 NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 402930
 Seq. ID LIB3431-058-P1-N1-A3
 Method BLASTN
 NCBI GI g1159878
 BLAST score 50
 E value 7.0e-19
 Match length 82
 % identity 90
 NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)

Seq. No. 402931
 Seq. ID LIB3431-058-P1-N1-A4
 Method BLASTN
 NCBI GI g2072554
 BLAST score 313
 E value 1.0e-175
 Match length 313
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 402932
 Seq. ID LIB3431-058-P1-N1-A5
 Method BLASTN
 NCBI GI g2570510
 BLAST score 131
 E value 2.0e-67
 Match length 267
 % identity 88
 NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 402933
 Seq. ID LIB3431-058-P1-N1-A7
 Method BLASTX
 NCBI GI g671740
 BLAST score 431
 E value 2.0e-42
 Match length 80
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402934
 Seq. ID LIB3431-058-P1-N1-B10
 Method BLASTX
 NCBI GI g3885886
 BLAST score 244
 E value 1.0e-22
 Match length 53

% identity 86
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402935
Seq. ID LIB3431-058-P1-N1-B11
Method BLASTX
NCBI GI g2582381
BLAST score 144
E value 1.0e-08
Match length 31
% identity 87
NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No. 402936
Seq. ID LIB3431-058-P1-N1-B12
Method BLASTX
NCBI GI g115793
BLAST score 396
E value 2.0e-38
Match length 78
% identity 95
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]

Seq. No. 402937
Seq. ID LIB3431-058-P1-N1-B2
Method BLASTX
NCBI GI g3924605
BLAST score 227
E value 8.0e-19
Match length 53
% identity 72
NCBI Description (AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]

Seq. No. 402938
Seq. ID LIB3431-058-P1-N1-B5
Method BLASTX
NCBI GI g115813
BLAST score 201
E value 2.0e-15
Match length 46
% identity 83
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402939
Seq. ID LIB3431-058-P1-N1-B6
Method BLASTX
NCBI GI g4038663
BLAST score 282
E value 4.0e-38

Match length 95
 % identity 77
 NCBI Description (AB020929) ribulose-1,5-bisphosphate carboxylase/oxygenase
 small subunit [Aegilops speltoides]

Seq. No. 402940
 Seq. ID LIB3431-058-P1-N1-B7
 Method BLASTN
 NCBI GI g21838
 BLAST score 67
 E value 3.0e-29
 Match length 207
 % identity 84
 NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase

Seq. No. 402941
 Seq. ID LIB3431-058-P1-N1-B8
 Method BLASTX
 NCBI GI g115813
 BLAST score 265
 E value 6.0e-23
 Match length 97
 % identity 61
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
 CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III
 chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402942
 Seq. ID LIB3431-058-P1-N1-B9
 Method BLASTX
 NCBI GI g132105
 BLAST score 396
 E value 2.0e-38
 Match length 73
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402943
 Seq. ID LIB3431-058-P1-N1-C1
 Method BLASTX
 NCBI GI g2191138
 BLAST score 390
 E value 1.0e-37
 Match length 91
 % identity 78
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis
 thaliana]

Seq. No. 402944

E value 0.0e+00
 Match length 495
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 402955
 Seq. ID LIB3431-058-P1-N1-D4
 Method BLASTN
 NCBI GI g438246
 BLAST score 57
 E value 5.0e-23
 Match length 77
 % identity 94
 NCBI Description S.tuberosum mRNA for glycine hydroxymethyltransferase

Seq. No. 402956
 Seq. ID LIB3431-058-P1-N1-D6
 Method BLASTX
 NCBI GI g131400
 BLAST score 276
 E value 2.0e-35
 Match length 113
 % identity 62
 NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
 >gi_81471_pir_S00409 photosystem II 10K protein precursor
 - spinach >gi_170127 (J03887) 10kd polypeptide precursor
 [Spinacia oleracea]

Seq. No. 402957
 Seq. ID LIB3431-058-P1-N1-D7
 Method BLASTX
 NCBI GI g3334149
 BLAST score 206
 E value 4.0e-22
 Match length 64
 % identity 91
 NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
 (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2323329 (AF014053) Mg
 protoporphyrin chelatase subunit [Nicotiana tabacum]

Seq. No. 402958
 Seq. ID LIB3431-058-P1-N1-D8
 Method BLASTX
 NCBI GI g693920
 BLAST score 416
 E value 1.0e-40
 Match length 80
 % identity 97
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No. 402959
 Seq. ID LIB3431-058-P1-N1-E1
 Method BLASTX
 NCBI GI g400989
 BLAST score 544

E value 1.0e-55
 Match length 137
 % identity 73
 NCBI Description 50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)
 >gi_322771_pir_A45113 ribosomal protein L24 precursor -
 common tobacco >gi_170273 (M87838) ribosomal protein L24
 [Nicotiana tabacum] >gi_170324 (M87839) ribosomal protein
 L24 [Nicotiana tabacum]

Seq. No. 402960
 Seq. ID LIB3431-058-P1-N1-E10
 Method BLASTX
 NCBI GI g482311
 BLAST score 502
 E value 1.0e-50
 Match length 99
 % identity 99
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
 (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
 complex protein 1 [Oryza sativa]

Seq. No. 402961
 Seq. ID LIB3431-058-P1-N1-E12
 Method BLASTN
 NCBI GI g20243
 BLAST score 145
 E value 1.0e-75
 Match length 169
 % identity 95
 NCBI Description O.sativa GP28 gene (partial)

Seq. No. 402962
 Seq. ID LIB3431-058-P1-N1-E2
 Method BLASTN
 NCBI GI g303858
 BLAST score 68
 E value 9.0e-30
 Match length 147
 % identity 87
 NCBI Description Rice mRNA for brain specific protein (S94 gene), complete
 cds

Seq. No. 402963
 Seq. ID LIB3431-058-P1-N1-E4
 Method BLASTX
 NCBI GI g132105
 BLAST score 289
 E value 4.0e-49
 Match length 97
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 402964
Seq. ID LIB3431-058-P1-N1-E5
Method BLASTX
NCBI GI g132105
BLAST score 325
E value 2.0e-47
Match length 94
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 402965
Seq. ID LIB3431-058-P1-N1-E7
Method BLASTX
NCBI GI g115794
BLAST score 439
E value 1.0e-66
Match length 134
% identity 92
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
protein type III precursor (cab-13) - tomato
>gi_19277_emb_CAA42818_ (X60275) LHCII type III
[Lycopersicon esculentum]

Seq. No. 402966
Seq. ID LIB3431-058-P1-N1-F11
Method BLASTX
NCBI GI g2245106
BLAST score 328
E value 2.0e-30
Match length 80
% identity 70
NCBI Description (Z97343) thioesterase like protein [Arabidopsis thaliana]

Seq. No. 402967
Seq. ID LIB3431-058-P1-N1-F12
Method BLASTX
NCBI GI g3885894
BLAST score 517
E value 2.0e-52
Match length 115
% identity 87
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 402968
Seq. ID LIB3431-058-P1-N1-F2

```
Method          BLASTX
NCBI GI         g2501190
BLAST score     325
E value        6.0e-30
Match length    85
% identity      81
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
                 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                 [Zea mays]
```

```
Seq. No.          402969
Seq. ID           LIB3431-058-P1-N1-F3
Method            BLASTX
NCBI GI           g115871
BLAST score       236
E value           2.0e-31
Match length      103
% identity        60
NCBI Description  [Segment 2 of 2] SERINE CARBOXYPEPTIDASE II CHAINS A AND B
                  (CARBOXYPEPTIDASE D) (CPDW-II) (CP-WII)
                  >gi_82623_pir_B29639 serine-type carboxypeptidase (EC
                  3.4.16.1) II B chain - wheat >gi_1421108_pdb_1BCR_B Chain
                  B, Complex Of The Wheat Serine Carboxypeptidase, Cpdw-Ii,
                  With The Microbial Peptide Aldehyde Inhibitor, Antipain,
                  And Arginine At Room Temperature >gi_1421113_pdb_1BCS_B
                  Chain B, Complex Of The Wheat Serine Carboxypeptidase,
                  Cpdw-Ii, With The Microbial Peptide Aldehyde Inhibitor,
                  Chymostatin, And Arginine At 100 Degrees Kelvin
                  >gi_226041_prf_1408164B CPase II B [Triticum aestivum]
```

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Seq. No.          402970
Seq. ID           LIB3431-058-P1-N1-F4
Method            BLASTX
NCBI GI           g3158476
BLAST score       217
E value           8.0e-31
Match length      89
% identity        78
NCBI Description   (AF067185) aquaporin 2 [Samanea saman]
```

Seq. No.	402971
Seq. ID	LIB3431-058-P1-N1-F5
Method	BLASTX
NCBI GI	g4960154
BLAST score	318
E value	4.0e-29
Match length	73
% identity	85
NCBI Description	(AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]

```
Seq. No.          402972
Seq. ID          LIB3431-058-P1-N1-F6
Method           BLASTN
NCBI GI          g505134
BLAST score      209
```

E value 1.0e-114
 Match length 305
 % identity 93
 NCBI Description Rice mRNA for ferredoxin, complete cds

Seq. No. 402973
 Seq. ID LIB3431-058-P1-N1-F8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 411
 E value 4.0e-54
 Match length 113
 % identity 96
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402974
 Seq. ID LIB3431-058-P1-N1-G1
 Method BLASTX
 NCBI GI g417260
 BLAST score 255
 E value 1.0e-24
 Match length 79
 % identity 69
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402975
 Seq. ID LIB3431-058-P1-N1-G10
 Method BLASTX
 NCBI GI g517500
 BLAST score 301
 E value 2.0e-27
 Match length 89
 % identity 70
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
 protein [Zea mays] >gi_444338_prf_1906386A photosystem II
 OE17 protein [Pisum sativum]

Seq. No. 402976
 Seq. ID LIB3431-058-P1-N1-G12
 Method BLASTX
 NCBI GI g417260
 BLAST score 411
 E value 5.0e-40
 Match length 128
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402977
 Seq. ID LIB3431-058-P1-N1-G4
 Method BLASTX
 NCBI GI g3885892
 BLAST score 513
 E value 4.0e-52

Match length 96
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402978
 Seq. ID LIB3431-058-P1-N1-G8
 Method BLASTX
 NCBI GI g548603
 BLAST score 543
 E value 1.0e-55
 Match length 108
 % identity 95
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
 barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 402979
 Seq. ID LIB3431-058-P1-N1-G9
 Method BLASTX
 NCBI GI g3004565
 BLAST score 188
 E value 2.0e-18
 Match length 94
 % identity 52
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 402980
 Seq. ID LIB3431-058-P1-N1-H11
 Method BLASTX
 NCBI GI g132105
 BLAST score 234
 E value 4.0e-21
 Match length 70
 % identity 81
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402981
 Seq. ID LIB3431-058-P1-N1-H2
 Method BLASTX
 NCBI GI g3789954
 BLAST score 339
 E value 1.0e-54
 Match length 110
 % identity 95
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 402982

Seq. ID LIB3431-058-P1-N1-H8
Method BLASTX
NCBI GI g132105
BLAST score 482
E value 2.0e-48
Match length 99
% identity 89
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402983
Seq. ID LIB3431-058-P1-N1-H9
Method BLASTX
NCBI GI g2407279
BLAST score 206
E value 4.0e-16
Match length 43
% identity 98
NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 402984
Seq. ID LIB3431-059-P1-K1-A10
Method BLASTX
NCBI GI g115787
BLAST score 571
E value 4.0e-59
Match length 111
% identity 98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402985
Seq. ID LIB3431-059-P1-K1-A11
Method BLASTX
NCBI GI g6006871
BLAST score 333
E value 4.0e-31
Match length 126
% identity 52
NCBI Description (AC009540) hypothetical protein [Arabidopsis thaliana] >gi_6091753_gb_AAF03463.1 AC009327_2 (AC009327) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402986
Seq. ID LIB3431-059-P1-K1-A12
Method BLASTX
NCBI GI g3789952

E value	2.0e-15
Match length	123
% identity	38
NCBI Description	(AC009853) unknown protein [Arabidopsis thaliana]
Seq. No.	402997
Seq. ID	LIB3431-059-P1-K1-B3
Method	BLASTX
NCBI GI	g131192
BLAST score	297
E value	6.0e-27
Match length	97
% identity	65
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir_S20937 photosystem I chain V precursor - barley >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide PSI-G precursor [Hordeum vulgare]
Seq. No.	402998
Seq. ID	LIB3431-059-P1-K1-B4
Method	BLASTX
NCBI GI	g3618310
BLAST score	334
E value	3.0e-31
Match length	97
% identity	67
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]
Seq. No.	402999
Seq. ID	LIB3431-059-P1-K1-B5
Method	BLASTX
NCBI GI	g1881585
BLAST score	231
E value	4.0e-19
Match length	117
% identity	45
NCBI Description	(U72489) remorin [Solanum tuberosum]
Seq. No.	403000
Seq. ID	LIB3431-059-P1-K1-B6
Method	BLASTX
NCBI GI	g2293480
BLAST score	168
E value	2.0e-12
Match length	48
% identity	73
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]
Seq. No.	403001
Seq. ID	LIB3431-059-P1-K1-B7
Method	BLASTX
NCBI GI	g3885894
BLAST score	402
E value	3.0e-39
Match length	91
% identity	87

000101" 9T048960

NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 403002
Seq. ID LIB3431-059-P1-K1-B8
Method BLASTX
NCBI GI g1351270
BLAST score 562
E value 7.0e-58
Match length 123
% identity 89
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_478410_pir_JQ2255 triose-phosphate isomerase (EC
5.3.1.1) - rice >gi_169821 (M87064) triosephosphate
isomerase [Oryza sativa]

Seq. No. 403003
Seq. ID LIB3431-059-P1-K1-B9
Method BLASTX
NCBI GI g4732091
BLAST score 254
E value 7.0e-22
Match length 69
% identity 67
NCBI Description (AF126742) bundle sheath defective protein 2 [Zea mays]

Seq. No. 403004
Seq. ID LIB3431-059-P1-K1-C1
Method BLASTN
NCBI GI g3617841
BLAST score 190
E value 1.0e-103
Match length 190
% identity 100
NCBI Description Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete
cds

Seq. No. 403005
Seq. ID LIB3431-059-P1-K1-C10
Method BLASTX
NCBI GI g132105
BLAST score 614
E value 6.0e-64
Match length 132
% identity 88
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 403006
Seq. ID LIB3431-059-P1-K1-C11
Method BLASTN

Match length	97
% identity	88
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.	403012
Seq. ID	LIB3431-059-P1-K1-C9
Method	BLASTX
NCBI GI	g3138799
BLAST score	603
E value	1.0e-62
Match length	125
% identity	92
NCBI Description	(AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
Seq. No.	403013
Seq. ID	LIB3431-059-P1-K1-D10
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	403014
Seq. ID	LIB3431-059-P1-K1-D11
Method	BLASTX
NCBI GI	g671740
BLAST score	695
E value	2.0e-73
Match length	128
% identity	99
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	403015
Seq. ID	LIB3431-059-P1-K1-D12
Method	BLASTX
NCBI GI	g3915826
BLAST score	309
E value	2.0e-28
Match length	67
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L5
Seq. No.	403016
Seq. ID	LIB3431-059-P1-K1-D3
Method	BLASTX
NCBI GI	g548605
BLAST score	386
E value	3.0e-37
Match length	80
% identity	95
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

Method BLASTX
 NCBI GI g1800227
 BLAST score 246
 E value 6.0e-21
 Match length 67
 % identity 60
 NCBI Description (U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]

Seq. No. 403036
 Seq. ID LIB3431-059-P1-K1-F4
 Method BLASTX
 NCBI GI g115787
 BLAST score 519
 E value 7.0e-53
 Match length 120
 % identity 87
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 403037
 Seq. ID LIB3431-059-P1-K1-F5
 Method BLASTX
 NCBI GI g132105
 BLAST score 395
 E value 2.0e-38
 Match length 73
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403038
 Seq. ID LIB3431-059-P1-K1-F6
 Method BLASTN
 NCBI GI g3819345
 BLAST score 60
 E value 7.0e-25
 Match length 168
 % identity 84
 NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0803

Seq. No. 403039
 Seq. ID LIB3431-059-P1-K1-G2
 Method BLASTX
 NCBI GI g132105
 BLAST score 429
 E value 2.0e-42
 Match length 104

000101-910100

Match length 67
 % identity 82
 NCBI Description (X66012) cathepsin B [Triticum aestivum]

Seq. No. 403045
 Seq. ID LIB3431-059-P1-K1-H12
 Method BLASTX
 NCBI GI g4567283
 BLAST score 270
 E value 8.0e-24
 Match length 125
 % identity 46
 NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 403046
 Seq. ID LIB3431-059-P1-K1-H2
 Method BLASTX
 NCBI GI g2582822
 BLAST score 213
 E value 6.0e-17
 Match length 53
 % identity 74
 NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No. 403047
 Seq. ID LIB3431-059-P1-K1-H4
 Method BLASTX
 NCBI GI g115772
 BLAST score 298
 E value 1.0e-34
 Match length 96
 % identity 83
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 403048
 Seq. ID LIB3431-059-P1-K1-H5
 Method BLASTX
 NCBI GI g871931
 BLAST score 281
 E value 4.0e-25
 Match length 77
 % identity 78
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 403049
 Seq. ID LIB3431-059-P1-K1-H7
 Method BLASTX
 NCBI GI g131773
 BLAST score 583
 E value 2.0e-60
 Match length 122
 % identity 97

E value 1.0e-123
 Match length 248
 % identity 98
 NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein (OsGRP1)

Seq. No. 403066
 Seq. ID LIB3431-059-P1-N1-B7
 Method BLASTX
 NCBI GI g3885894
 BLAST score 193
 E value 1.0e-14
 Match length 53
 % identity 75
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 403067
 Seq. ID LIB3431-059-P1-N1-B8
 Method BLASTX
 NCBI GI g1351270
 BLAST score 195
 E value 6.0e-15
 Match length 48
 % identity 85
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_478410_pir_JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No. 403068
 Seq. ID LIB3431-059-P1-N1-C1
 Method BLASTN
 NCBI GI g3617841
 BLAST score 186
 E value 1.0e-100
 Match length 190
 % identity 99
 NCBI Description Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete cds

Seq. No. 403069
 Seq. ID LIB3431-059-P1-N1-C10
 Method BLASTX
 NCBI GI g347451
 BLAST score 197
 E value 3.0e-15
 Match length 37
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 403070
 Seq. ID LIB3431-059-P1-N1-C12
 Method BLASTX
 NCBI GI g3885892
 BLAST score 266
 E value 3.0e-23

Method BLASTN
 NCBI GI g2072554
 BLAST score 380
 E value 0.0e+00
 Match length 380
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403077
 Seq. ID LIB3431-059-P1-N1-D11
 Method BLASTX
 NCBI GI g671740
 BLAST score 243
 E value 1.0e-20
 Match length 47
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 403078
 Seq. ID LIB3431-059-P1-N1-D12
 Method BLASTX
 NCBI GI g3915826
 BLAST score 202
 E value 9.0e-16
 Match length 41
 % identity 100
 NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 403079
 Seq. ID LIB3431-059-P1-N1-D3
 Method BLASTX
 NCBI GI g548605
 BLAST score 386
 E value 2.0e-37
 Match length 80
 % identity 95
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 403080
 Seq. ID LIB3431-059-P1-N1-D4
 Method BLASTX
 NCBI GI g132105
 BLAST score 526
 E value 1.0e-53
 Match length 95
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

Match length 102
 % identity 86
 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
 >gi_2119068_pir_S58630 ribosomal protein S7 - maize
 chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
 protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
 ribosomal protein S7 [Zea mays]

Seq. No. 403091
 Seq. ID LIB3431-059-P1-N1-E7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 286
 E value 1.0e-25
 Match length 65
 % identity 85
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 403092
 Seq. ID LIB3431-059-P1-N1-E9
 Method BLASTX
 NCBI GI g733454
 BLAST score 232
 E value 3.0e-19
 Match length 48
 % identity 94
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
 [Zea mays]

Seq. No. 403093
 Seq. ID LIB3431-059-P1-N1-F1
 Method BLASTX
 NCBI GI g1173347
 BLAST score 216
 E value 2.0e-17
 Match length 47
 % identity 94
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
 (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
 >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
 (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
 aestivum]

Seq. No. 403094
 Seq. ID LIB3431-059-P1-N1-F10
 Method BLASTX
 NCBI GI g2754849
 BLAST score 199
 E value 2.0e-15
 Match length 45
 % identity 87
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase
 [Fritillaria agrestis]

Seq. No. 403095
 Seq. ID LIB3431-059-P1-N1-F4

```
Method          BLASTX
NCBI GI         g3036951
BLAST score      199
E value         9.0e-19
Match length     52
% identity       98
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana glauca]
```

```
Seq. No.      403096
Seq. ID      LIB3431-059-P1-N1-F5
Method       BLASTX
NCBI GI      g671740
BLAST score   336
E value      2.0e-31
Match length  64
% identity    95
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

```
Seq. No.          403097
Seq. ID           LIB3431-059-P1-N1-F7
Method            BLASTN
NCBI GI           g606816
BLAST score       306
E value           1.0e-172
Match length      326
% identity        98
NCBI Description   Oryza sativa chloroplast carbonic anhydrase mRNA, complete
                  cds
```

```
Seq. No.          403098
Seq. ID          LIB3431-059-P1-N1-F8
Method           BLASTX
NCBI GI          g517500
BLAST score      378
E value          2.0e-36
Match length     91
% identity       81
NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
protein [Zea mays] >gi_444338_prf__1906386A photosystem II
OE17 protein [Pisum sativum]
```

```
Seq. No.          403099
Seq. ID           LIB3431-059-P1-N1-G11
Method            BLASTX
NCBI GI           g4079798
BLAST score       326
E value           3.0e-30
Match length      65
% identity        97
NCBI Description  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
```

```
Seq. No.      403100
Seq. ID      LIB3431-059-P1-N1-G2
Method       BLASTX
```


E value 2.0e-48
 Match length 112
 % identity 86
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 403122
 Seq. ID LIB3431-060-P1-K1-B7
 Method BLASTX
 NCBI GI g320618
 BLAST score 510
 E value 8.0e-52
 Match length 113
 % identity 86
 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 403123
 Seq. ID LIB3431-060-P1-K1-B9
 Method BLASTX
 NCBI GI g3023816
 BLAST score 592
 E value 2.0e-61
 Match length 115
 % identity 98
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No. 403124
 Seq. ID LIB3431-060-P1-K1-C1
 Method BLASTX
 NCBI GI g3885888
 BLAST score 348
 E value 8.0e-33
 Match length 113
 % identity 67
 NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 403125
 Seq. ID LIB3431-060-P1-K1-C10
 Method BLASTX
 NCBI GI g5091623
 BLAST score 295
 E value 1.0e-26
 Match length 75
 % identity 69
 NCBI Description (AC007454) Similar to gb_U93048 somatic embryogenesis receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

[Hordeum vulgare]

Seq. No. 403136
 Seq. ID LIB3431-060-P1-K1-D7
 Method BLASTN
 NCBI GI g20239
 BLAST score 141
 E value 3.0e-73
 Match length 169
 % identity 96
 NCBI Description O.sativa (rice) shoot-specific GOS5 gene for a putative chloroplast transit peptide

Seq. No. 403137
 Seq. ID LIB3431-060-P1-K1-D8
 Method BLASTX
 NCBI GI g4587579
 BLAST score 251
 E value 2.0e-21
 Match length 143
 % identity 35
 NCBI Description (AC006550) F1003.1 [Arabidopsis thaliana]

Seq. No. 403138
 Seq. ID LIB3431-060-P1-K1-D9
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 4.0e-11
 Match length 44
 % identity 64
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403139
 Seq. ID LIB3431-060-P1-K1-E1
 Method BLASTX
 NCBI GI g4559358
 BLAST score 341
 E value 5.0e-32
 Match length 97
 % identity 63
 NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No. 403140
 Seq. ID LIB3431-060-P1-K1-E10
 Method BLASTX
 NCBI GI g1488297
 BLAST score 190
 E value 3.0e-14
 Match length 132
 % identity 36
 NCBI Description (U63530) osRAD23 [Oryza sativa]

Seq. No. 403141
 Seq. ID LIB3431-060-P1-K1-E2
 Method BLASTX

Seq. No. 403159
 Seq. ID LIB3431-060-P1-K1-G3
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 403160
 Seq. ID LIB3431-060-P1-K1-G5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 700
 E value 4.0e-74
 Match length 131
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 403161
 Seq. ID LIB3431-060-P1-K1-G6
 Method BLASTX
 NCBI GI g2501189
 BLAST score 257
 E value 3.0e-22
 Match length 121
 % identity 58
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
 >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 403162
 Seq. ID LIB3431-060-P1-K1-G7
 Method BLASTX
 NCBI GI g4544428
 BLAST score 214
 E value 3.0e-17
 Match length 51
 % identity 76
 NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 403163
 Seq. ID LIB3431-060-P1-K1-G8
 Method BLASTX
 NCBI GI g1053047
 BLAST score 591
 E value 3.0e-61
 Match length 118
 % identity 100
 NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
 histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
 [Glycine max]

0000016-101000

Method BLASTX
 NCBI GI g132105
 BLAST score 567
 E value 2.0e-58
 Match length 122
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 403169
 Seq. ID LIB3431-060-P1-K1-H4
 Method BLASTX
 NCBI GI g2306981
 BLAST score 503
 E value 5.0e-51
 Match length 90
 % identity 98
 NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 403170
 Seq. ID LIB3431-060-P1-K1-H5
 Method BLASTX
 NCBI GI g2501189
 BLAST score 547
 E value 3.0e-56
 Match length 111
 % identity 95
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
 >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 403171
 Seq. ID LIB3431-060-P1-K1-H7
 Method BLASTX
 NCBI GI g3789952
 BLAST score 560
 E value 1.0e-57
 Match length 112
 % identity 98
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
 sativa]

Seq. No. 403172
 Seq. ID LIB3431-060-P1-K1-H9
 Method BLASTN
 NCBI GI g2062705
 BLAST score 35
 E value 4.0e-10
 Match length 35

Seq. No. 403183
 Seq. ID LIB3431-060-P1-N1-C12
 Method BLASTN
 NCBI GI g3789953
 BLAST score 298
 E value 1.0e-167
 Match length 298
 % identity 100
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 403184
 Seq. ID LIB3431-060-P1-N1-C2
 Method BLASTN
 NCBI GI g3885885
 BLAST score 144
 E value 3.0e-75
 Match length 167
 % identity 97
 NCBI Description Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA, complete cds

Seq. No. 403185
 Seq. ID LIB3431-060-P1-N1-C4
 Method BLASTN
 NCBI GI g2072554
 BLAST score 186
 E value 1.0e-100
 Match length 210
 % identity 97
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403186
 Seq. ID LIB3431-060-P1-N1-C6
 Method BLASTX
 NCBI GI g3885886
 BLAST score 630
 E value 9.0e-66
 Match length 112
 % identity 99
 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 403187
 Seq. ID LIB3431-060-P1-N1-C9
 Method BLASTX
 NCBI GI g3184292
 BLAST score 287
 E value 1.0e-25
 Match length 56
 % identity 86
 NCBI Description (AC004136) putative nucleic acid binding protein, 5' partial [Arabidopsis thaliana]

Seq. No. 403188

Seq. ID LIB3431-060-P1-N1-D1
 Method BLASTX
 NCBI GI g3913811
 BLAST score 367
 E value 4.0e-35
 Match length 91
 % identity 84
 NCBI Description GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
 >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA
 reductase [*Oryza sativa*]

Seq. No. 403189
 Seq. ID LIB3431-060-P1-N1-D12
 Method BLASTX
 NCBI GI g3126854
 BLAST score 345
 E value 1.0e-32
 Match length 65
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [*Oryza sativa*]

Seq. No. 403190
 Seq. ID LIB3431-060-P1-N1-D2
 Method BLASTX
 NCBI GI g266567
 BLAST score 306
 E value 8.0e-28
 Match length 87
 % identity 66
 NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
 (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
 >gi_421956_pir_S23558 mitochondrial processing peptidase
 (EC 3.4.99.41) alpha chain precursor - potato
 >gi_21493_emb_CAA46990_ (X66284) mitochondrial processing
 peptidase [*Solanum tuberosum*]

Seq. No. 403191
 Seq. ID LIB3431-060-P1-N1-D4
 Method BLASTX
 NCBI GI g733456
 BLAST score 352
 E value 2.0e-33
 Match length 73
 % identity 95
 NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
 [*Zea mays*]

Seq. No. 403192
 Seq. ID LIB3431-060-P1-N1-D8
 Method BLASTX
 NCBI GI g3850577
 BLAST score 185
 E value 6.0e-16
 Match length 120
 % identity 41
 NCBI Description (AC005278) This gene may be cut off. [*Arabidopsis thaliana*]


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NCBI GI      g5006852
BLAST score  225
E value      1.0e-123
Match length 293
% identity   94
NCBI Description  Oryza sativa homeodomain leucine zipper protein (hox4)
                  mRNA, complete cds

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Seq. No.          403204
Seq. ID           LIB3431-060-P1-N1-G2
Method            BLASTX
NCBI GI           g131192
BLAST score       209
E value           2.0e-16
Match length      44
% identity        86
NCBI Description   PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937
                   photosystem i chain V precursor - barley
                   >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide
                   PSI-G precursor [Hordeum vulgare]

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Seq. No.      403205
Seq. ID      LIB3431-060-P1-N1-G3
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      1.0e-19
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
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Seq. No.      403206
Seq. ID      LIB3431-060-P1-N1-G5
Method       BLASTX
NCBI GI      g132105
BLAST score   186
E value      6.0e-14
Match length  35
% identity    100
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
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Seq. No.      403207
Seq. ID      LIB3431-060-P1-N1-G7
Method       BLASTX
NCBI GI      g4544428
BLAST score  294
```

E value 2.0e-26
 Match length 81
 % identity 69
 NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 403208
 Seq. ID LIB3431-060-P1-N1-G8
 Method BLASTX
 NCBI GI g417103
 BLAST score 283
 E value 4.0e-25
 Match length 58
 % identity 98
 NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone H3.3-like protein - Arabidopsis thaliana
 >gi_16324_emb_CAA42957_(X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_(X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_(X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_(X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1 (AP000559) EST D15300 (C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]

Seq. No. 403209
 Seq. ID LIB3431-060-P1-N1-H10
 Method BLASTX
 NCBI GI g671740
 BLAST score 499
 E value 2.0e-50
 Match length 91
 % identity 99
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 403210
 Seq. ID LIB3431-060-P1-N1-H11
 Method BLASTX
 NCBI GI g3036951
 BLAST score 282
 E value 3.0e-25
 Match length 54
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]

Method BLASTX
 NCBI GI g132105
 BLAST score 327
 E value 8.0e-41
 Match length 108
 % identity 83
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403217
 Seq. ID LIB3431-061-P1-K1-A11
 Method BLASTX
 NCBI GI g3345477
 BLAST score 232
 E value 2.0e-19
 Match length 85
 % identity 55
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 403218
 Seq. ID LIB3431-061-P1-K1-A12
 Method BLASTX
 NCBI GI g82080
 BLAST score 310
 E value 1.0e-28
 Match length 90
 % identity 68
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 403219
 Seq. ID LIB3431-061-P1-K1-A2
 Method BLASTX
 NCBI GI g4455248
 BLAST score 150
 E value 1.0e-09
 Match length 69
 % identity 51
 NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]

Seq. No. 403220
 Seq. ID LIB3431-061-P1-K1-A3
 Method BLASTX
 NCBI GI g3913018
 BLAST score 570
 E value 7.0e-59
 Match length 115
 % identity 100
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
aldolase [Oryza sativa]

Seq. No. 403221
Seq. ID LIB3431-061-P1-K1-A4
Method BLASTN
NCBI GI g20262
BLAST score 330
E value 0.0e+00
Match length 346
% identity 99
NCBI Description O.sativa light-induced mRNA

Seq. No. 403222
Seq. ID LIB3431-061-P1-K1-A6
Method BLASTX
NCBI GI g2351846
BLAST score 146
E value 3.0e-09
Match length 123
% identity 30
NCBI Description (U93050) poly(A) binding protein II [Mus musculus]

Seq. No. 403223
Seq. ID LIB3431-061-P1-K1-A8
Method BLASTN
NCBI GI g3063523
BLAST score 176
E value 2.0e-94
Match length 219
% identity 95
NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small
subunit mRNA, complete cds

Seq. No. 403224
Seq. ID LIB3431-061-P1-K1-A9
Method BLASTX
NCBI GI g1709846
BLAST score 163
E value 4.0e-11
Match length 118
% identity 45
NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
22 kDa component of photosystem II [Lycopersicon
esculentum]

Seq. No. 403225
Seq. ID LIB3431-061-P1-K1-B10
Method BLASTX
NCBI GI g115813
BLAST score 243
E value 1.0e-20
Match length 55
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 403226
 Seq. ID LIB3431-061-P1-K1-B11
 Method BLASTX
 NCBI GI g4165550
 BLAST score 567
 E value 1.0e-58
 Match length 121
 % identity 88
 NCBI Description (AJ004915) apgm [Malus domestica]

Seq. No. 403227
 Seq. ID LIB3431-061-P1-K1-B2
 Method BLASTX
 NCBI GI g320618
 BLAST score 477
 E value 5.0e-48
 Match length 106
 % identity 85
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 403228
 Seq. ID LIB3431-061-P1-K1-B3
 Method BLASTX
 NCBI GI g3913192
 BLAST score 142
 E value 9.0e-09
 Match length 70
 % identity 47
 NCBI Description CYTOCHROME P450 93A1 >gi_2129824_pir_S62899 cytochrome
 P450 (CYP93 A1) - soybean >gi_1232111_dbj_BAA12159_
 (D83968) Cytochrome P-450 (CYP93A1) [Glycine max]
 >gi_1588679_prf_2209281A cytochrome P450 [Glycine max]

Seq. No. 403229
 Seq. ID LIB3431-061-P1-K1-B4
 Method BLASTX
 NCBI GI g400879
 BLAST score 202
 E value 6.0e-16
 Match length 102
 % identity 48
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
 (PSI-N) >gi_479690_pir_S35159 photosystem I chain psaN -
 barley >gi_19095_emb_CAA47056_ (X66428) photosystem I
 subunit N [Hordeum vulgare]

Seq. No. 403230
 Seq. ID LIB3431-061-P1-K1-B7
 Method BLASTX
 NCBI GI g733454
 BLAST score 431
 E value 1.0e-42

09564016-101000

Match length 103
% identity 81
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 403231
Seq. ID LIB3431-061-P1-K1-C10
Method BLASTX
NCBI GI g4586058
BLAST score 209
E value 2.0e-17
Match length 116
% identity 46
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 403232
Seq. ID LIB3431-061-P1-K1-C12
Method BLASTN
NCBI GI g2072554
BLAST score 47
E value 3.0e-17
Match length 199
% identity 81
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
cds

Seq. No. 403233
Seq. ID LIB3431-061-P1-K1-C2
Method BLASTX
NCBI GI g1052960
BLAST score 748
E value 1.0e-79
Match length 146
% identity 91
NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 403234
Seq. ID LIB3431-061-P1-K1-C3
Method BLASTN
NCBI GI g1304214
BLAST score 51
E value 1.0e-19
Match length 95
% identity 88
NCBI Description Rice mRNA for precursor of 22 kDa protein of photosystem II
(PSII-S), complete cds

Seq. No. 403235
Seq. ID LIB3431-061-P1-K1-C4
Method BLASTX
NCBI GI g729668
BLAST score 197
E value 3.0e-15
Match length 58
% identity 60
NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1,
drought-inducible - Lycopersicon pennellii >gi_436823

Seq. ID LIB3431-061-P1-K1-E6
 Method BLASTX
 NCBI GI g115787
 BLAST score 552
 E value 1.0e-56
 Match length 105
 % identity 99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 403256
 Seq. ID LIB3431-061-P1-K1-E8
 Method BLASTX
 NCBI GI g1881585
 BLAST score 187
 E value 5.0e-14
 Match length 44
 % identity 80
 NCBI Description (U72489) remorin [Solanum tuberosum]

Seq. No. 403257
 Seq. ID LIB3431-061-P1-K1-E9
 Method BLASTX
 NCBI GI g401190
 BLAST score 669
 E value 2.0e-70
 Match length 128
 % identity 96
 NCBI Description THAUMATIN-LIKE PROTEIN PRECURSOR >gi_100715_pir_S25551 thaumatin-like protein - rice >gi_20376_emb_CAA48278_ (X68197) thaumatin-like protein [Oryza sativa]

Seq. No. 403258
 Seq. ID LIB3431-061-P1-K1-F10
 Method BLASTX
 NCBI GI g3775987
 BLAST score 430
 E value 2.0e-42
 Match length 112
 % identity 71
 NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No. 403259
 Seq. ID LIB3431-061-P1-K1-F11
 Method BLASTX
 NCBI GI g131225
 BLAST score 311
 E value 1.0e-28
 Match length 105
 % identity 65
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

09684016 to 303000

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Seq. No.          403282
Seq. ID           LIB3431-061-P1-K1-H7
Method            BLASTX
NCBI GI           g1483213
BLAST score       308
E value           4.0e-28
Match length      108
% identity        56
NCBI Description   (X96480) PAC [Arabidopsis thaliana]
                   >gi_5729705_gb_AAD48512.1_AC007927_2 (AC007927) pale cress
                   protein [Arabidopsis thaliana]
```

```
Seq. No.      403283
Seq. ID      LIB3431-061-P1-K1-H9
Method       BLASTX
NCBI GI      g3075488
BLAST score   705
E value      1.0e-74
Match length  137
% identity    99
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
```

```
Seq. No.      403284
Seq. ID      LIB3431-062-P1-K1-A1
Method       BLASTX
NCBI GI      g3885888
BLAST score   321
E value      1.0e-29
Match length  108
% identity    66
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
```

```
Seq. No.      403285
Seq. ID       LIB3431-062-P1-K1-A10
Method        BLASTX
NCBI GI       g3929545
BLAST score   425
E value       9.0e-42
Match length  107
% identity    84
NCBI Description (AF067194) S-adenosylmethionine decarboxylase [Oryza
```

sativa]

Seq. No. 403286
 Seq. ID LIB3431-062-P1-K1-A12
 Method BLASTX
 NCBI GI g5360591
 BLAST score 476
 E value 9.0e-48
 Match length 149
 % identity 60
 NCBI Description (AB022328) nClpP3 [Arabidopsis thaliana]

Seq. No. 403287
 Seq. ID LIB3431-062-P1-K1-A2
 Method BLASTX
 NCBI GI g419742
 BLAST score 624
 E value 3.0e-65
 Match length 127
 % identity 91
 NCBI Description protochlorophyllide reductase (EC 1.3.1.33) precursor -
 loblolly pine

Seq. No. 403288
 Seq. ID LIB3431-062-P1-K1-A3
 Method BLASTX
 NCBI GI g548603
 BLAST score 434
 E value 7.0e-43
 Match length 130
 % identity 70
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
 barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 403289
 Seq. ID LIB3431-062-P1-K1-A7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 180
 E value 9.0e-14
 Match length 44
 % identity 80
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 403290
 Seq. ID LIB3431-062-P1-K1-A8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 648
 E value 1.0e-73
 Match length 150
 % identity 93
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403291

BLAST score 204
 E value 6.0e-16
 Match length 130
 % identity 45
 NCBI Description (AB023482) ESTs AU058081(E30812), AU058365(E50679), AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome 37kD subunit.(X96974) [Oryza sativa]

Seq. No. 403302
 Seq. ID LIB3431-062-P1-K1-C5
 Method BLASTX
 NCBI GI g132105
 BLAST score 553
 E value 7.0e-57
 Match length 120
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403303
 Seq. ID LIB3431-062-P1-K1-C6
 Method BLASTX
 NCBI GI g1854378
 BLAST score 252
 E value 1.0e-25
 Match length 125
 % identity 56
 NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No. 403304
 Seq. ID LIB3431-062-P1-K1-C7
 Method BLASTX
 NCBI GI g4972111
 BLAST score 546
 E value 6.0e-56
 Match length 151
 % identity 62
 NCBI Description (AL078579) protein phosphatase homolog (PPH1) [Arabidopsis thaliana]

Seq. No. 403305
 Seq. ID LIB3431-062-P1-K1-C9
 Method BLASTN
 NCBI GI g2072554
 BLAST score 188
 E value 1.0e-101
 Match length 196
 % identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403306
 Seq. ID LIB3431-062-P1-K1-D1
 Method BLASTN
 NCBI GI g2267594
 BLAST score 49
 E value 4.0e-19
 Match length 49
 % identity 100

NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds

Seq. No. 403307
 Seq. ID LIB3431-062-P1-K1-D11
 Method BLASTX
 NCBI GI g1835731
 BLAST score 461
 E value 5.0e-46
 Match length 95
 % identity 95

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 403308
 Seq. ID LIB3431-062-P1-K1-D12
 Method BLASTX
 NCBI GI g2244965
 BLAST score 307
 E value 3.0e-28
 Match length 85
 % identity 68

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403309
 Seq. ID LIB3431-062-P1-K1-D2
 Method BLASTN
 NCBI GI g6015437
 BLAST score 35
 E value 3.0e-10
 Match length 35
 % identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403310
 Seq. ID LIB3431-062-P1-K1-D3
 Method BLASTX
 NCBI GI g21695
 BLAST score 361
 E value 3.0e-34
 Match length 110
 % identity 62

NCBI Description (X66014) cathepsin B [Triticum aestivum]

Seq. No. 403311
 Seq. ID LIB3431-062-P1-K1-D4
 Method BLASTX
 NCBI GI g4585882

BLAST score 444
E value 2.0e-45
Match length 141
% identity 70
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
[Arabidopsis thaliana]

Seq. No. 403312
Seq. ID LIB3431-062-P1-K1-D5
Method BLASTX
NCBI GI g3290022
BLAST score 434
E value 9.0e-43
Match length 142
% identity 58
NCBI Description (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol)
lyase; plastidic isoform [Solanum tuberosum]

Seq. No. 403313
Seq. ID LIB3431-062-P1-K1-D7
Method BLASTX
NCBI GI g3201969
BLAST score 225
E value 2.0e-18
Match length 43
% identity 98
NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No. 403314
Seq. ID LIB3431-062-P1-K1-E1
Method BLASTN
NCBI GI g2624325
BLAST score 86
E value 9.0e-41
Match length 110
% identity 95
NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein
(OsGRP1)

Seq. No. 403315
Seq. ID LIB3431-062-P1-K1-E11
Method BLASTN
NCBI GI g218209
BLAST score 155
E value 1.0e-81
Match length 281
% identity 96
NCBI Description Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS2106

Seq. No. 403316
Seq. ID LIB3431-062-P1-K1-E12
Method BLASTX
NCBI GI g3618310
BLAST score 331
E value 6.0e-31

Match length 109
 % identity 46
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 403322
 Seq. ID LIB3431-062-P1-K1-E8
 Method BLASTN
 NCBI GI g5042437
 BLAST score 287
 E value 1.0e-160
 Match length 358
 % identity 99
 NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 403323
 Seq. ID LIB3431-062-P1-K1-F1
 Method BLASTX
 NCBI GI g4079798
 BLAST score 227
 E value 4.0e-20
 Match length 92
 % identity 60
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 403324
 Seq. ID LIB3431-062-P1-K1-F10
 Method BLASTX
 NCBI GI g132105
 BLAST score 270
 E value 4.0e-24
 Match length 79
 % identity 71
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403325
 Seq. ID LIB3431-062-P1-K1-F11
 Method BLASTX
 NCBI GI g5042462
 BLAST score 221
 E value 9.0e-18
 Match length 109
 % identity 47
 NCBI Description (AC007789) putative negatively light-regulated protein [Oryza sativa]

Seq. No. 403326
 Seq. ID LIB3431-062-P1-K1-F12
 Method BLASTX

Seq. No. 403331
 Seq. ID LIB3431-062-P1-K1-G1
 Method BLASTX
 NCBI GI g2462834
 BLAST score 293
 E value 3.0e-26
 Match length 106
 % identity 57
 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403332
 Seq. ID LIB3431-062-P1-K1-G10
 Method BLASTN
 NCBI GI g1835730
 BLAST score 156
 E value 1.0e-82
 Match length 164
 % identity 99
 NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 403333
 Seq. ID LIB3431-062-P1-K1-G11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 289
 E value 2.0e-26
 Match length 57
 % identity 98
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403334
 Seq. ID LIB3431-062-P1-K1-G12
 Method BLASTX
 NCBI GI g3885892
 BLAST score 667
 E value 3.0e-70
 Match length 136
 % identity 94
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 403335
 Seq. ID LIB3431-062-P1-K1-G2
 Method BLASTX
 NCBI GI g5031281
 BLAST score 356
 E value 1.0e-33
 Match length 121
 % identity 60
 NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 403336
 Seq. ID LIB3431-062-P1-K1-G3
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237

E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 403337
 Seq. ID LIB3431-062-P1-K1-G4
 Method BLASTX
 NCBI GI g5123711
 BLAST score 467
 E value 1.0e-46
 Match length 148
 % identity 62
 NCBI Description (AL079347) putative protein [Arabidopsis thaliana]

Seq. No. 403338
 Seq. ID LIB3431-062-P1-K1-G5
 Method BLASTX
 NCBI GI g132105
 BLAST score 751
 E value 6.0e-80
 Match length 164
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 403339
 Seq. ID LIB3431-062-P1-K1-G6
 Method BLASTX
 NCBI GI g4973264
 BLAST score 376
 E value 4.0e-36
 Match length 93
 % identity 73
 NCBI Description (AF144391) thioredoxin-like 5 [Arabidopsis thaliana]

Seq. No. 403340
 Seq. ID LIB3431-062-P1-K1-G7
 Method BLASTX
 NCBI GI g3913018
 BLAST score 515
 E value 3.0e-52
 Match length 125
 % identity 81
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
 (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
 aldolase [Oryza sativa]

Seq. No. 403341
 Seq. ID LIB3431-062-P1-K1-G8
 Method BLASTN
 NCBI GI g20369
 BLAST score 388
 E value 0.0e+00
 Match length 396
 % identity 99
 NCBI Description Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31)
 >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase

Seq. No. 403342
 Seq. ID LIB3431-062-P1-K1-H2
 Method BLASTX
 NCBI GI g3289002
 BLAST score 590
 E value 4.0e-61
 Match length 170
 % identity 42
 NCBI Description (AF073522) CRP1 [Zea mays]

Seq. No. 403343
 Seq. ID LIB3431-062-P1-K1-H5
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 403344
 Seq. ID LIB3431-062-P1-K1-H7
 Method BLASTX
 NCBI GI g132105
 BLAST score 606
 E value 5.0e-63
 Match length 131
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403345
 Seq. ID LIB3431-062-P1-K1-H9
 Method BLASTN
 NCBI GI g6015437

BLAST score 162
 E value 6.0e-86
 Match length 282
 % identity 89
 NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,
 complete cds

Seq. No. 403351
 Seq. ID LIB3431-062-P1-N1-A8
 Method BLASTX
 NCBI GI g2570513
 BLAST score 172
 E value 2.0e-12
 Match length 32
 % identity 97
 NCBI Description (AF022739) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 403352
 Seq. ID LIB3431-062-P1-N1-A9
 Method BLASTX
 NCBI GI g4138290
 BLAST score 313
 E value 1.0e-28
 Match length 63
 % identity 97
 NCBI Description (AJ005841) thioredoxin M [Oryza sativa]

Seq. No. 403353
 Seq. ID LIB3431-062-P1-N1-B1
 Method BLASTX
 NCBI GI g5931625
 BLAST score 529
 E value 6.0e-54
 Match length 111
 % identity 94
 NCBI Description (AB032761) rab5B [Oryza sativa]

Seq. No. 403354
 Seq. ID LIB3431-062-P1-N1-B10
 Method BLASTX
 NCBI GI g482311
 BLAST score 398
 E value 1.0e-38
 Match length 79
 % identity 100
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
 (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
 complex protein 1 [Oryza sativa]

Seq. No. 403355
 Seq. ID LIB3431-062-P1-N1-B11
 Method BLASTX
 NCBI GI g3158476
 BLAST score 166
 E value 2.0e-11
 Match length 43
 % identity 70

E value 1.0e-123
 Match length 352
 % identity 91
 NCBI Description Oryza sativa ferredoxin mRNA, complete cds

Seq. No. 403362
 Seq. ID LIB3431-062-P1-N1-B9
 Method BLASTX
 NCBI GI g132105
 BLAST score 411
 E value 4.0e-40
 Match length 76
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403363
 Seq. ID LIB3431-062-P1-N1-C11
 Method BLASTX
 NCBI GI g115787
 BLAST score 403
 E value 3.0e-39
 Match length 76
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 403364
 Seq. ID LIB3431-062-P1-N1-C12
 Method BLASTN
 NCBI GI g20262
 BLAST score 108
 E value 1.0e-53
 Match length 220
 % identity 87
 NCBI Description O.sativa light-induced mRNA

Seq. No. 403365
 Seq. ID LIB3431-062-P1-N1-C5
 Method BLASTN
 NCBI GI g218207
 BLAST score 256
 E value 1.0e-142
 Match length 284
 % identity 98
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS1139

Seq. No. 403366
 Seq. ID LIB3431-062-P1-N1-C6
 Method BLASTX
 NCBI GI g1854378
 BLAST score 275
 E value 4.0e-24
 Match length 60
 % identity 87
 NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No. 403367
 Seq. ID LIB3431-062-P1-N1-C7
 Method BLASTX
 NCBI GI g3643090
 BLAST score 337
 E value 2.0e-31
 Match length 96
 % identity 66
 NCBI Description (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No. 403368
 Seq. ID LIB3431-062-P1-N1-C8
 Method BLASTX
 NCBI GI g451193
 BLAST score 397
 E value 2.0e-38
 Match length 109
 % identity 72
 NCBI Description (L28008) wali7 [Triticum aestivum]
 >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]

Seq. No. 403369
 Seq. ID LIB3431-062-P1-N1-C9
 Method BLASTN
 NCBI GI g2072554
 BLAST score 317
 E value 1.0e-178
 Match length 325
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403370
 Seq. ID LIB3431-062-P1-N1-D1
 Method BLASTN
 NCBI GI g2267594
 BLAST score 43
 E value 1.0e-15
 Match length 43
 % identity 100
 NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds

Seq. No. 403371

Seq. ID LIB3431-062-P1-N1-D11
 Method BLASTX
 NCBI GI g131400
 BLAST score 243
 E value 3.0e-27
 Match length 93
 % identity 67
 NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
 >gi_81471_pir_S00409 photosystem II 10K protein precursor
 - spinach >gi_170127 (J03887) 10kd polypeptide precursor
 [Spinacia oleracea]

Seq. No. 403372
 Seq. ID LIB3431-062-P1-N1-D12
 Method BLASTX
 NCBI GI g2244965
 BLAST score 157
 E value 2.0e-10
 Match length 37
 % identity 81
 NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403373
 Seq. ID LIB3431-062-P1-N1-D3
 Method BLASTN
 NCBI GI g21692
 BLAST score 43
 E value 9.0e-15
 Match length 75
 % identity 89
 NCBI Description T.aestivum mRNA 1 for cathepsin B (2529)

Seq. No. 403374
 Seq. ID LIB3431-062-P1-N1-D4
 Method BLASTX
 NCBI GI g115813
 BLAST score 280
 E value 8.0e-25
 Match length 68
 % identity 82
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
 CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III
 chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 403375
 Seq. ID LIB3431-062-P1-N1-D5
 Method BLASTX
 NCBI GI g399333
 BLAST score 289
 E value 8.0e-26
 Match length 66
 % identity 88
 NCBI Description CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYL SERINE
 SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE)
 >gi_322740_pir_A43407 cysteine synthase (EC 4.2.99.8)
 precursor - pepper >gi_17944_emb_CAA46086 (X64874)
 O-acetylserine (thiol)-lyase [Capsicum annuum]

BLAST score 193
 E value 1.0e-14
 Match length 35
 % identity 100
 NCBI Description (AF094775) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 403392
 Seq. ID LIB3431-062-P1-N1-F9
 Method BLASTX
 NCBI GI g132105
 BLAST score 556
 E value 3.0e-57
 Match length 101
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403393
 Seq. ID LIB3431-062-P1-N1-G1
 Method BLASTX
 NCBI GI g2462834
 BLAST score 244
 E value 1.0e-20
 Match length 107
 % identity 48
 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403394
 Seq. ID LIB3431-062-P1-N1-G10
 Method BLASTX
 NCBI GI g1835731
 BLAST score 426
 E value 6.0e-42
 Match length 92
 % identity 89
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 403395
 Seq. ID LIB3431-062-P1-N1-G11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 370
 E value 2.0e-35
 Match length 70
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403396
 Seq. ID LIB3431-062-P1-N1-G12

Method BLASTX
 NCBI GI g3885892
 BLAST score 208
 E value 1.0e-16
 Match length 41
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 403397
 Seq. ID LIB3431-062-P1-N1-G2
 Method BLASTX
 NCBI GI g5031281
 BLAST score 223
 E value 4.0e-18
 Match length 47
 % identity 81
 NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 403398
 Seq. ID LIB3431-062-P1-N1-G3
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 403399
 Seq. ID LIB3431-062-P1-N1-G4
 Method BLASTX
 NCBI GI g5123711
 BLAST score 280
 E value 9.0e-25
 Match length 90
 % identity 61
 NCBI Description (AL079347) putative protein [Arabidopsis thaliana]

Seq. No. 403400
 Seq. ID LIB3431-062-P1-N1-G5
 Method BLASTX
 NCBI GI g347451
 BLAST score 220
 E value 9.0e-18
 Match length 65
 % identity 69
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 403401
 Seq. ID LIB3431-062-P1-N1-G6
 Method BLASTX
 NCBI GI g4973264
 BLAST score 376
 E value 4.0e-36

09684015 "101000

Match length 93
% identity 73
NCBI Description (AF144391) thioredoxin-like 5 [Arabidopsis thaliana]

Seq. No. 403402
Seq. ID LIB3431-062-P1-N1-G7
Method BLASTX
NCBI GI g2407279
BLAST score 206
E value 4.0e-16
Match length 42
% identity 100
NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 403403
Seq. ID LIB3431-062-P1-N1-G8
Method BLASTN
NCBI GI g20369
BLAST score 381
E value 0.0e+00
Match length 385
% identity 100
NCBI Description Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31)
>gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase

Seq. No. 403404
Seq. ID LIB3431-062-P1-N1-G9
Method BLASTN
NCBI GI g3885887
BLAST score 269
E value 1.0e-149
Match length 397
% identity 92
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 403405
Seq. ID LIB3431-062-P1-N1-H11
Method BLASTX
NCBI GI g451193
BLAST score 412
E value 3.0e-40
Match length 114
% identity 72
NCBI Description (L28008) wali7 [Triticum aestivum]
>gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]

Seq. No. 403406
Seq. ID LIB3431-062-P1-N1-H3
Method BLASTX
NCBI GI g3250697
BLAST score 377
E value 3.0e-36
Match length 91
% identity 76

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 403407
 Seq. ID LIB3431-062-P1-N1-H5
 Method BLASTN
 NCBI GI g2072554
 BLAST score 285
 E value 1.0e-159
 Match length 301
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403408
 Seq. ID LIB3431-062-P1-N1-H7
 Method BLASTX
 NCBI GI g132105
 BLAST score 402
 E value 4.0e-39
 Match length 73
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403409
 Seq. ID LIB3431-062-P1-N1-H9
 Method BLASTN
 NCBI GI g5051932
 BLAST score 200
 E value 1.0e-108
 Match length 254
 % identity 100
 NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds

Seq. No. 403410
 Seq. ID LIB3431-063-P1-K1-A1
 Method BLASTN
 NCBI GI g6015437
 BLAST score 41
 E value 1.0e-13
 Match length 41
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403411
 Seq. ID LIB3431-063-P1-K1-A11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 7.0e-20

Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 403412
 Seq. ID LIB3431-063-P1-K1-A12
 Method BLASTX
 NCBI GI g3126854
 BLAST score 392
 E value 2.0e-38
 Match length 74
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403413
 Seq. ID LIB3431-063-P1-K1-A2
 Method BLASTX
 NCBI GI g132105
 BLAST score 363
 E value 1.0e-34
 Match length 101
 % identity 74
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 403414
 Seq. ID LIB3431-063-P1-K1-A3
 Method BLASTX
 NCBI GI g2407281
 BLAST score 696
 E value 1.0e-73
 Match length 144
 % identity 93
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 403415
 Seq. ID LIB3431-063-P1-K1-A4
 Method BLASTN
 NCBI GI g3819202
 BLAST score 51
 E value 2.0e-19
 Match length 191
 % identity 82
 NCBI Description Hordeum vulgare partial mRNA; clone cMWG0680.rev

Seq. No. 403416
 Seq. ID LIB3431-063-P1-K1-A5

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403421
Seq. ID LIB3431-063-P1-K1-B10
Method BLASTX
NCBI GI g4220533
BLAST score 220
E value 2.0e-18
Match length 56
% identity 77
NCBI Description (AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No. 403422
Seq. ID LIB3431-063-P1-K1-B11
Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 1.0e-12
Match length 38
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403423
Seq. ID LIB3431-063-P1-K1-B2
Method BLASTX
NCBI GI g3929924
BLAST score 479
E value 4.0e-48
Match length 93
% identity 98
NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 403424
Seq. ID LIB3431-063-P1-K1-B3
Method BLASTX
NCBI GI g4103987
BLAST score 486
E value 6.0e-49
Match length 115
% identity 83
NCBI Description (AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589)
5,10-methylenetetrahydrofolate dehydrogenase:
5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No. 403425
Seq. ID LIB3431-063-P1-K1-B5
Method BLASTX
NCBI GI g2570511
BLAST score 256
E value 2.0e-22
Match length 57

```
% identity      88
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
```

Seq. No.	403426
Seq. ID	LIB3431-063-P1-K1-B6
Method	BLASTN
NCBI GI	g20177
BLAST score	47
E value	1.0e-17
Match length	115
% identity	85
NCBI Description	Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

```
Seq. No.      403427
Seq. ID      LIB3431-063-P1-K1-B8
Method       BLASTX
NCBI GI      g3126854
BLAST score   434
E value      5.0e-43
Match length  84
% identity   98
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      403428
Seq. ID      LIB3431-063-P1-K1-B9
Method       BLASTX
NCBI GI      g5803266
BLAST score   425
E value      7.0e-42
Match length  84
% identity    99
NCBI Description (AP000399) ESTs AU078063(S15496),C97608(C60475),
C28255(C60475) correspond to a region of the predicted
gene; similar to plastid transketolase 2 (Y15782) [Oryza
sativa]
```

```
Seq. No..      403429
Seq. ID        LIB3431-063-P1-K1-C1
Method         BLASTX
NCBI GI        g2245120
BLAST score    372
E value        1.0e-35
Match length   121
% identity     60
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	403430
Seq. ID	LIB3431-063-P1-K1-C11
Method	BLASTX
NCBI GI	g2264373
BLAST score	163
E value	1.0e-11
Match length	41
% identity	66
NCBI Description	(AC002354) putative NAM/no apical meristem protein [Arabidopsis thaliana]

Match length 77
 % identity 95
 NCBI Description *Oryza sativa* glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 403436
 Seq. ID LIB3431-063-P1-K1-D10
 Method BLASTX
 NCBI GI g4038695
 BLAST score 198
 E value 3.0e-18
 Match length 63
 % identity 78
 NCBI Description (AB020945) ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [*Avena sativa*]

Seq. No. 403437
 Seq. ID LIB3431-063-P1-K1-D11
 Method BLASTX
 NCBI GI g132105
 BLAST score 518
 E value 6.0e-53
 Match length 99
 % identity 95
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [*Oryza sativa*] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza sativa*] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [*Oryza sativa*]

Seq. No. 403438
 Seq. ID LIB3431-063-P1-K1-D2
 Method BLASTX
 NCBI GI g5734636
 BLAST score 238
 E value 5.0e-20
 Match length 71
 % identity 56
 NCBI Description (AP000391) Similar to putative lipase (AC006232) [*Oryza sativa*]

Seq. No. 403439
 Seq. ID LIB3431-063-P1-K1-D5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 159
 E value 3.0e-11
 Match length 39
 % identity 79
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza sativa*]

Seq. No. 403440
 Seq. ID LIB3431-063-P1-K1-D6

Method BLASTX
 NCBI GI g6014934
 BLAST score 540
 E value 3.0e-55
 Match length 118
 % identity 81
 NCBI Description DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS AND LEAVES PROTEIN) >gi_1305531 (U55219) defective chloroplasts and leaves; required for chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi_1323698 (U55278) DCL [Solanum lycopersicum]

Seq. No. 403441
 Seq. ID LIB3431-063-P1-K1-D9
 Method BLASTX
 NCBI GI g3549665
 BLAST score 175
 E value 1.0e-12
 Match length 37
 % identity 81
 NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403442
 Seq. ID LIB3431-063-P1-K1-E11
 Method BLASTX
 NCBI GI g3738329
 BLAST score 257
 E value 2.0e-22
 Match length 65
 % identity 75
 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 403443
 Seq. ID LIB3431-063-P1-K1-E4
 Method BLASTN
 NCBI GI g451192
 BLAST score 47
 E value 1.0e-17
 Match length 119
 % identity 85
 NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds

Seq. No. 403444
 Seq. ID LIB3431-063-P1-K1-E6
 Method BLASTX
 NCBI GI g3914423
 BLAST score 183
 E value 8.0e-14
 Match length 37
 % identity 84
 NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]

Seq. No. 403445
 Seq. ID LIB3431-063-P1-K1-E7
 Method BLASTN
 NCBI GI g6015437

BLAST score 35
 E value 2.0e-10
 Match length 35
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403446
 Seq. ID LIB3431-063-P1-K1-E8
 Method BLASTX
 NCBI GI g2182029
 BLAST score 522
 E value 2.0e-53
 Match length 99
 % identity 96
 NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No. 403447
 Seq. ID LIB3431-063-P1-K1-E9
 Method BLASTN
 NCBI GI g473980
 BLAST score 45
 E value 1.0e-16
 Match length 73
 % identity 89
 NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene

Seq. No. 403448
 Seq. ID LIB3431-063-P1-K1-F10
 Method BLASTX
 NCBI GI g2130069
 BLAST score 788
 E value 2.0e-84
 Match length 143
 % identity 99
 NCBI Description catalase (EC 1.11.1.6) catA - rice
 >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 403449
 Seq. ID LIB3431-063-P1-K1-F11
 Method BLASTX
 NCBI GI g2244867
 BLAST score 314
 E value 9.0e-29
 Match length 156
 % identity 40
 NCBI Description (Z97337) hydroxynitrile lyase like protein [Arabidopsis thaliana]

Seq. No. 403450
 Seq. ID LIB3431-063-P1-K1-F12
 Method BLASTX
 NCBI GI g2570515
 BLAST score 568
 E value 1.0e-58
 Match length 121
 % identity 93
 NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	403466
Seq. ID	LIB3431-063-P1-K1-H4
Method	BLASTX
NCBI GI	g3832512
BLAST score	374
E value	5.0e-36
Match length	110
% identity	69
NCBI Description	(AF097922) granule-bound glycogen (starch) synthase [Astragalus membranaceus]

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Seq. No.      403467
Seq. ID       LIB3431-063-P1-K1-H5
Method        BLASTX
NCBI GI       g131225
BLAST score    179
E value       2.0e-13
Match length   59
% identity     66
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [Hordeum vulgare]
```

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Seq. No.          403468
Seq. ID           LIB3431-063-P1-N1-A11
Method            BLASTX
NCBI GI           g2072555
BLAST score       237
E value           7.0e-20
Match length      44
% identity        100
NCBI Description  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

```
Seq. No.      403469
Seq. ID       LIB3431-063-P1-N1-A12
Method        BLASTX
NCBI GI       g3126854
BLAST score    393
E value        5.0e-38
Match length   78
% identity     95
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

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Seq. No.          403470
Seq. ID           LIB3431-063-P1-N1-A2
Method            BLASTX
NCBI GI           g132105
BLAST score       508
E value           2.0e-51
Match length      91
% identity         100
NCBI Description  RIBULOSE BISPHOEPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

00000161000

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 403471
Seq. ID LIB3431-063-P1-N1-A3
Method BLASTX
NCBI GI g132105
BLAST score 713
E value 2.0e-75
Match length 131
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 403472
Seq. ID LIB3431-063-P1-N1-A4
Method BLASTX
NCBI GI g5541681
BLAST score 202
E value 9.0e-16
Match length 83
% identity 59
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]

Seq. No. 403473
Seq. ID LIB3431-063-P1-N1-A5
Method BLASTX
NCBI GI g548605
BLAST score 570
E value 9.0e-59
Match length 127
% identity 89
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[Hordeum vulgare]

Seq. No. 403474
Seq. ID LIB3431-063-P1-N1-A7
Method BLASTN
NCBI GI g2773153
BLAST score 373
E value 0.0e+00
Match length 389
% identity 99

Seq. ID	LIB3431-063-P1-N1-B9
Method	BLASTN
NCBI GI	g5803242
BLAST score	388
E value	0.0e+00
Match length	484
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

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Seq. No.      403485
Seq. ID       LIB3431-063-P1-N1-C12
Method        BLASTX
NCBI GI       g6103011
BLAST score    478
E value        5.0e-48
Match length   104
% identity     46
NCBI Description (X84225) precursor of photosystem II subunit (22KDa)
[Nicotiana tabacum]
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```
Seq. No.          403486
Seq. ID           LIB3431-063-P1-N1-C3
Method            BLASTX
NCBI GI           g871931
BLAST score       220
E value           8.0e-18
Match length      59
% identity        71
NCBI Description   (D30763) ferredoxin [Oryza sativa]
```

```
Seq. No.      403487
Seq. ID      LIB3431-063-P1-N1-C4
Method       BLASTX
NCBI GI      g132105
BLAST score   144
E value      5.0e-09
Match length  36
% identity    81
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.      403488
Seq. ID.      LIB3431-063-P1-N1-C9
Method        BLASTX
NCBI GI       g4098250
BLAST score    164
E value       3.0e-11
Match length   71
% identity     41
NCBI Description (U76611) similar to Solanum tuberosum ci21A gene product
```


Match length 96
 % identity 95
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 403505
 Seq. ID LIB3431-063-P1-N1-F9
 Method BLASTX
 NCBI GI g115802
 BLAST score 189
 E value 3.0e-14
 Match length 36
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
 >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No. 403506
 Seq. ID LIB3431-063-P1-N1-G1
 Method BLASTX
 NCBI GI g120668
 BLAST score 469
 E value 7.0e-47
 Match length 102
 % identity 88
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_82399_pir_A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
 >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347_prf_1301218A dehydrogenase, glyceraldehydophosphate [Hordeum vulgare var. distichum]

Seq. No. 403507
 Seq. ID LIB3431-063-P1-N1-G10
 Method BLASTX
 NCBI GI g21839
 BLAST score 595
 E value 7.0e-62
 Match length 118
 % identity 94
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 403508
 Seq. ID LIB3431-063-P1-N1-G11
 Method BLASTX
 NCBI GI g517500
 BLAST score 273
 E value 3.0e-24
 Match length 68
 % identity 81
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 403509

Seq. ID LIB3431-063-P1-N1-G12
 Method BLASTX
 NCBI GI g2407279
 BLAST score 398
 E value 1.0e-38
 Match length 75
 % identity 100
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 403510
 Seq. ID LIB3431-063-P1-N1-G2
 Method BLASTX
 NCBI GI g4138290
 BLAST score 283
 E value 3.0e-25
 Match length 55
 % identity 100
 NCBI Description (AJ005841) thioredoxin M [Oryza sativa]

Seq. No. 403511
 Seq. ID LIB3431-063-P1-N1-G7
 Method BLASTX
 NCBI GI g2191138
 BLAST score 275
 E value 3.0e-24
 Match length 84
 % identity 64
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No. 403512
 Seq. ID LIB3431-063-P1-N1-G8
 Method BLASTX
 NCBI GI g132105
 BLAST score 429
 E value 3.0e-42
 Match length 79
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403513
 Seq. ID LIB3431-063-P1-N1-H1
 Method BLASTX
 NCBI GI g693920
 BLAST score 419
 E value 5.0e-41
 Match length 80
 % identity 97
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum

0697016-301000

Seq. No.	403517
Seq. ID	LIB3431-063-P1-N1-H5
Method	BLASTX
NCBI GI	g131225
BLAST score	216
E value	2.0e-17
Match length	56
% identity	73

37-kDa subunit from Homo sapiens and is a member of PF_00004 ATPases associated with various cellular activities. [Arabidopsis thaliana]

Seq. No. 403523
 Seq. ID LIB3432-005-P1-K1-A3
 Method BLASTX
 NCBI GI g5912299
 BLAST score 587
 E value 7.0e-61
 Match length 123
 % identity 93
 NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

Seq. No. 403524
 Seq. ID LIB3432-006-P1-K1-B8
 Method BLASTX
 NCBI GI g871931
 BLAST score 492
 E value 8.0e-50
 Match length 116
 % identity 88
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 403525
 Seq. ID LIB3432-006-P1-K1-H9
 Method BLASTX
 NCBI GI g2827524
 BLAST score 215
 E value 2.0e-17
 Match length 44
 % identity 77
 NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 403526
 Seq. ID LIB3432-007-P1-K1-B6
 Method BLASTX
 NCBI GI g1244566
 BLAST score 719
 E value 3.0e-76
 Match length 145
 % identity 92
 NCBI Description (U39321) acetyl-CoA carboxylase [Triticum aestivum]
 >gi_1588584_prf__2208491A Ac-CoA carboxylase [Triticum aestivum]

Seq. No. 403527
 Seq. ID LIB3432-007-P1-K1-C1
 Method BLASTN
 NCBI GI g577352
 BLAST score 55
 E value 6.0e-22
 Match length 148
 % identity 38
 NCBI Description Streptococcus equi M protein (emmSzW60) gene, complete cds

Seq. No. 403528


```

NCBI GI      g3914603
BLAST score   317
E value       4.0e-29
Match length  145
% identity    50
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]

```

Seq. No.	403534
Seq. ID	LIB3432-009-P1-K1-A2
Method	BLASTX
NCBI GI	g3367594
BLAST score	194
E value	1.0e-14
Match length	70
% identity	53
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

```
Seq. No.      403535
Seq. ID       LIB3432-009-P1-K1-A7
Method        BLASTX
NCBI GI       g4574139
BLAST score    159
E value       2.0e-17
Match length   83
% identity     64
NCBI Description (AF073697) cysteine synthase [Oryza sativa]
```

```
Seq. No.      403536
Seq. ID      LIB3432-010-P1-K1-B11
Method       BLASTX
NCBI GI      g940288
BLAST score   381
E value      1.0e-36
Match length  137
% identity    57
NCBI Description (L43510) protein localized in the nucleoli of pea nuclei;
ORF; putative [Pisum sativum]
```

```
Seq. No.      403537
Seq. ID      LIB3432-010-P1-K1-G11
Method       BLASTX
NCBI GI      g606817
BLAST score   329
E value      2.0e-30
Match length  78
% identity    82
NCBI Description (U08404) carbonic anhydrase [Oryza sativa]
>gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
anhydrase 3 [Oryza sativa]
```

```
Seq. No.      403538
Seq. ID       LIB3432-010-P1-K1-G2
Method        BLASTX
NCBI GI       q2072555
```


Method	BLASTX
NCBI GI	g4455680
BLAST score	150
E value	4.0e-10
Match length	66
% identity	47
NCBI Description	(AL035472) putative prolyl tRNA synthetase [Mycobacterium leprae]

```
Seq. No.      403550
Seq. ID      LIB3432-013-P1-K1-H12
Method       BLASTX
NCBI GI      g2373403
BLAST score   157
E value      5.0e-11
Match length  42
% identity    67
NCBI Description (D85193) similar to the membrane protein RD28 [Arabidopsis thaliana]
```

```
Seq. No.      403551
Seq. ID      LIB3432-014-P1-K1-H6
Method       BLASTX
NCBI GI      g4006855
BLAST score   215
E value      2.0e-17
Match length  76
% identity    57
NCBI Description (Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]
```

```
Seq. No.      403552
Seq. ID      LIB3432-015-P1-K1-D5
Method       BLASTX
NCBI GI      g1173347
BLAST score   618
E value      1.0e-64
Match length  120
% identity    94
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
               (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
               >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
               3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
               (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
               aestivum]
```

Seq. No.	403553
Seq. ID	LIB3432-015-P1-K1-D6
Method	BLASTX
NCBI GI	g2281115
BLAST score	631
E value	6.0e-66
Match length	154
% identity	76
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCI TYPE II CAB) >gi_82243_pir_S00442 chlorophyll a/b-binding protein precursor - garden petunia >gi_169214 (M21317) chlorophyll binding protein precursor [Petunia hybrida] >gi_226259_prf_1503272A chlorophyll binding protein [Petunia sp.]

```
Seq. No.      403569
Seq. ID      LIB3432-022-P1-K1-E1
Method       BLASTX
NCBI GI      g166835
BLAST score   464
E value      1.0e-46
Match length  92
% identity    96
NCBI Description (M86720) ribulose biphosphate carboxylase/oxygenase
activase [Arabidopsis thaliana] >gi_2642170 (AC003000)
Rubisco activase [Arabidopsis thaliana]
```

Seq. No.	403570
Seq. ID	LIB3432-023-P1-K1-H11
Method	BLASTX
NCBI GI	g2754849
BLAST score	324
E value	6.0e-30
Match length	96
% identity	68
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

```
Seq. No.      403571
Seq. ID      LIB3432-024-P1-K1-B12
Method       BLASTX
NCBI GI      g132105
BLAST score   183
E value      6.0e-14
Match length  59
% identity    68
NCBI Description RIBULOSE BISPSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bispshosphate
                carboxylase S [Oryza sativa]
```

```
Seq. No.      403572
Seq. ID      LIB3432-024-P1-K1-H5
Method       BLASTX
NCBI GI      g1353352
BLAST score   191
E value      1.0e-14
Match length  57
% identity    61
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
```


(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 403578
 Seq. ID LIB3432-028-P1-K1-G5
 Method BLASTX
 NCBI GI g729535
 BLAST score 160
 E value 9.0e-11
 Match length 78
 % identity 46
 NCBI Description FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
 (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)
 (FTR-B)

Seq. No. 403579
 Seq. ID LIB3432-028-P1-K1-H3
 Method BLASTX
 NCBI GI g1217967
 BLAST score 438
 E value 3.0e-43
 Match length 124
 % identity 72
 NCBI Description (X96431) high affinity sulphate transporter [Hordeum
 vulgare]

Seq. No. 403580
 Seq. ID LIB3432-029-P1-K1-E3
 Method BLASTN
 NCBI GI g5803242
 BLAST score 221
 E value 1.0e-121
 Match length 334
 % identity 97
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No. 403581
 Seq. ID LIB3432-030-P1-K1-A1
 Method BLASTN
 NCBI GI g1835730
 BLAST score 129
 E value 3.0e-66
 Match length 285
 % identity 88
 NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,
 complete cds

Seq. No. 403582
 Seq. ID LIB3432-030-P1-K1-A11
 Method BLASTN
 NCBI GI g1835730

000001-97048950

Seq. ID	LIB3432-034-P2-K1-H5
Method	BLASTX
NCBI GI	g5007084
BLAST score	696
E value	1.0e-73
Match length	133
% identity	98
NCBI Description	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]
Seq. No.	403588
Seq. ID	LIB3432-034-P2-K1-H6
Method	BLASTX
NCBI GI	g4895183
BLAST score	272
E value	6.0e-24
Match length	105
% identity	49
NCBI Description	(AC007661) hypothetical protein [Arabidopsis thaliana]
Seq. No.	403589
Seq. ID	LIB3432-035-P2-K1-A2
Method	BLASTN
NCBI GI	g304219
BLAST score	70
E value	3.0e-31
Match length	173
% identity	86
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds
Seq. No.	403590
Seq. ID	LIB3432-035-P2-K1-A3
Method	BLASTX
NCBI GI	g3913018
BLAST score	819
E value	6.0e-88
Match length	163
% identity	96
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]
Seq. No.	403591
Seq. ID	LIB3432-035-P2-K1-C7
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	2.0e-10
Match length	35
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.	403592
Seq. ID	LIB3432-035-P2-K1-G6
Method	BLASTX
NCBI GI	g132081

000101"91043560

BLAST score 167
E value 3.0e-13
Match length 73
% identity 55
NCBI Description (AJ006752) starch synthase, isoform V [Vigna unguiculata]

Seq. No. 403598
Seq. ID LIB3432-037-P1-K1-E3
Method BLASTX
NCBI GI g4850330
BLAST score 332
E value 7.0e-31
Match length 63
% identity 100
NCBI Description (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]

Seq. No. 403599
Seq. ID LIB3432-037-P1-K1-F7
Method BLASTX
NCBI GI g2773154
BLAST score 217
E value 6.0e-18
Match length 71
% identity 62
NCBI Description (AF039573) abscisic acid- and stress-inducible protein [Oryza sativa]

Seq. No. 403600
Seq. ID LIB3432-039-P1-K1-A2
Method BLASTX
NCBI GI g3122572
BLAST score 519
E value 8.0e-53
Match length 148
% identity 67
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No. 403601
Seq. ID LIB3432-039-P1-K1-G6
Method BLASTX
NCBI GI g5091509
BLAST score 719
E value 3.0e-76
Match length 134
% identity 100
NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

Seq. No. 403602
Seq. ID LIB3432-039-P1-K1-H12
Method BLASTN

Seq. ID LIB3432-042-P2-K1-A9
 Method BLASTX
 NCBI GI g2662310
 BLAST score 219
 E value 3.0e-18
 Match length 66
 % identity 67
 NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 403613
 Seq. ID LIB3432-042-P2-K1-B2
 Method BLASTX
 NCBI GI g3643607
 BLAST score 260
 E value 8.0e-23
 Match length 62
 % identity 76
 NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 403614
 Seq. ID LIB3432-042-P2-K1-B3
 Method BLASTX
 NCBI GI g2129675
 BLAST score 555
 E value 4.0e-57
 Match length 122
 % identity 89
 NCBI Description probable chlorophyll synthetase G4 - Arabidopsis thaliana
 >gi_972938 (U19382) putative chlorophyll synthetase
 [Arabidopsis thaliana] >gi_3068709 (AF049236) putative
 chlorophyll synthetase [Arabidopsis thaliana]

Seq. No. 403615
 Seq. ID LIB3432-042-P2-K1-B4
 Method BLASTN
 NCBI GI g167086
 BLAST score 52
 E value 2.0e-20
 Match length 148
 % identity 84
 NCBI Description Hordeum vulgare photosystem I protein (PSI-L) mRNA,
 complete cds

Seq. No. 403616
 Seq. ID LIB3432-042-P2-K1-B7
 Method BLASTX
 NCBI GI g82080
 BLAST score 200
 E value 7.0e-16
 Match length 72
 % identity 60
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 403617
 Seq. ID LIB3432-042-P2-K1-C11


```
Seq. ID      LIB3432-042-P2-K1-G10
Method       BLASTX
NCBI GI      g3212852
BLAST score   329
E value      9.0e-31
Match length  111
% identity    64
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      403632
Seq. ID      LIB3432-042-P2-K1-G4
Method       BLASTX
NCBI GI      g82080
BLAST score   533
E value      2.0e-54
Match length  131
% identity    74
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                >gi_226872_prf_1609235A chlorophyll a/b binding protein
                [Lycopersicon esculentum]
```

Seq. No.	403633
Seq. ID	LIB3432-042-P2-K1-G5
Method	BLASTN
NCBI GI	g4733953
BLAST score	36
E value	9.0e-11
Match length	72
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F13011 genomic sequence, complete sequence

```

Seq. No.          403634
Seq. ID           LIB3432-042-P2-K1-G7
Method            BLASTX
NCBI GI           g115772
BLAST score       571
E value           4.0e-59
Match length      114
% identity        95
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                  CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi_20178_emb_CAA32108
                  (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                  [Oryza sativa]

```

Seq. No.	403635
Seq. ID	LIB3432-042-P2-K1-H2
Method	BLASTX
NCBI GI	g2072727
BLAST score	425
E value	3.0e-42
Match length	82
% identity	98
NCBI Description	(Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No. 403636

Seq. ID LIB3432-043-P1-K1-G3
 Method BLASTX
 NCBI GI g3582333
 BLAST score 147
 E value 7.0e-10
 Match length 57
 % identity 58
 NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403641
 Seq. ID LIB3432-043-P1-K1-H12
 Method BLASTN
 NCBI GI g6063530
 BLAST score 402
 E value 0.0e+00
 Match length 414
 % identity 99
 NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No. 403642
 Seq. ID LIB3432-043-P1-K1-H6
 Method BLASTX
 NCBI GI g1929998
 BLAST score 333
 E value 3.0e-31
 Match length 89
 % identity 78
 NCBI Description (U77463) NADPH-dependent HC-toxin reductase [Hordeum vulgare]

Seq. No. 403643
 Seq. ID LIB3432-044-P1-K1-B8
 Method BLASTX
 NCBI GI g2570511
 BLAST score 280
 E value 6.0e-25
 Match length 110
 % identity 72
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 403644
 Seq. ID LIB3432-044-P1-K1-C2
 Method BLASTX
 NCBI GI g435942
 BLAST score 383
 E value 5.0e-37
 Match length 107
 % identity 71
 NCBI Description (U04295) DNA-binding factor of bZIP class [Oryza sativa]

Seq. No. 403645
 Seq. ID LIB3432-044-P1-K1-G1
 Method BLASTX
 NCBI GI g3885884
 BLAST score 371
 E value 1.0e-35
 Match length 103

```

% identity      73
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.       403646
Seq. ID        LIB3432-044-P1-K1-H1
Method         BLASTX
NCBI GI        g5912424
BLAST score    512
E value        5.0e-52
Match length   150
% identity     71
NCBI Description (AJ242970) BTF3b-like factor [Arabidopsis thaliana]

Seq. No.       403647
Seq. ID        LIB3432-045-P1-K1-A8
Method         BLASTX
NCBI GI        g3367536
BLAST score    296
E value        5.0e-27
Match length   77
% identity     77
NCBI Description (AC004392) Contains similarity to symbiosis-related like
protein F1N20.80 gi_2961343 from A. thaliana BAC
gb_AL022140. EST gb_T04695 comes from this gene.
[Arabidopsis thaliana]

Seq. No.       403648
Seq. ID        LIB3432-045-P1-K1-B1
Method         BLASTX
NCBI GI        g804973
BLAST score    147
E value        3.0e-09
Match length   48
% identity     62
NCBI Description (X81376) L-ascorbate peroxidase [Capsicum annuum]

Seq. No.       403649
Seq. ID        LIB3432-045-P1-K1-G2
Method         BLASTX
NCBI GI        g4056502
BLAST score    414
E value        1.0e-40
Match length   105
% identity     75
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.       403650
Seq. ID        LIB3432-045-P1-K1-G3
Method         BLASTX
NCBI GI        g2911358
BLAST score    521
E value        5.0e-53
Match length   142
% identity     70
NCBI Description (AF041043) NADPH HC toxin reductase [Zea mays]

Seq. No.       403651

```


NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403661
Seq. ID LIB3432-050-P1-K1-A7
Method BLASTX
NCBI GI g4115379
BLAST score 254
E value 9.0e-22
Match length 116
% identity 45
NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No. 403662
Seq. ID LIB3432-050-P1-K1-E3
Method BLASTX
NCBI GI g2754849
BLAST score 227
E value 3.0e-19
Match length 52
% identity 85
NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No. 403663
Seq. ID LIB3432-051-P1-K1-A2
Method BLASTN
NCBI GI g4158220
BLAST score 45
E value 3.0e-16
Match length 49
% identity 98
NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide

Seq. No. 403664
Seq. ID LIB3432-051-P1-K1-D1
Method BLASTX
NCBI GI g132105
BLAST score 168
E value 3.0e-12
Match length 50
% identity 68
NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 403665
Seq. ID LIB3432-051-P1-K1-D9
Method BLASTX
NCBI GI g4519671
BLAST score 353
E value 3.0e-33
Match length 127
% identity 61
NCBI Description (AB017693) transfactor [Nicotiana tabacum]

Seq. No. 403666
Seq. ID LIB3432-051-P1-K1-E10
Method BLASTX
NCBI GI g3913641
BLAST score 290
E value 2.0e-26
Match length 63
% identity 92
NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
>gi_3041777_dbj_BAA25423_ (AB007194)
fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 403667
Seq. ID LIB3432-051-P1-K1-G8
Method BLASTN
NCBI GI g3885891
BLAST score 79
E value 8.0e-37
Match length 114
% identity 93
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
mRNA, complete cds

Seq. No. 403668
Seq. ID LIB3432-052-P1-K1-D7
Method BLASTX
NCBI GI g2921158
BLAST score 228
E value 9.0e-19
Match length 73
% identity 66
NCBI Description (AF022909) ClpC [Arabidopsis thaliana]

Seq. No. 403669
Seq. ID LIB3432-052-P1-K1-F9
Method BLASTX
NCBI GI g5306242
BLAST score 204
E value 5.0e-16
Match length 46
% identity 78
NCBI Description (AC006438) unknown protein [Arabidopsis thaliana]

E value 1.0e-62
 Match length 159
 % identity 72
 NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403676
 Seq. ID LIB3432-058-P1-K1-C10
 Method BLASTN
 NCBI GI g21843
 BLAST score 43
 E value 4.0e-15
 Match length 73
 % identity 90
 NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II

Seq. No. 403677
 Seq. ID LIB3432-058-P1-K1-G5
 Method BLASTX
 NCBI GI g1805654
 BLAST score 265
 E value 5.0e-23
 Match length 101
 % identity 49
 NCBI Description (X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No. 403678
 Seq. ID LIB3432-058-P1-K1-G6
 Method BLASTX
 NCBI GI g2765081
 BLAST score 636
 E value 5.0e-71
 Match length 154
 % identity 84
 NCBI Description (Y10557) g5bf [Arabidopsis thaliana]

Seq. No. 403679
 Seq. ID LIB3432-058-P1-K1-H5
 Method BLASTX
 NCBI GI g548605
 BLAST score 401
 E value 2.0e-39
 Match length 90
 % identity 89
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 403680
 Seq. ID LIB3432-059-P1-K1-A8
 Method BLASTX
 NCBI GI g3914466
 BLAST score 440
 E value 1.0e-43

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Seq. No.      403691
Seq. ID      LIB3432-060-P1-K1-H6
Method       BLASTX
NCBI GI      g3868756
BLAST score   509
E value      6.0e-52
Match length  95
% identity    95
NCBI Description (D86611) catalase [Oryza sativa]
```

```
Seq. No.      403692
Seq. ID      LIB3433-001-P1-K1-D5
Method       BLASTX
NCBI GI      g2739366
BLAST score   167
E value      6.0e-12
Match length  67
% identity   49
NCBI Description (AC002505) SF16 like protein [Arabidopsis thaliana]
```

```
Seq. No.      403694
Seq. ID      LIB3433-001-P1-K1-F12
Method       BLASTX
NCBI GI      g3540195
BLAST score   250
E value      2.0e-21
Match length  108
% identity    27
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
```

51946

Match length 52
 % identity 81
 NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 403706
 Seq. ID LIB3433-005-Q6-K1-D12
 Method BLASTX
 NCBI GI g1729971
 BLAST score 199
 E value 9.0e-16
 Match length 71
 % identity 59
 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
 (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
 rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
 sativa]

Seq. No. 403707
 Seq. ID LIB3433-005-Q6-K1-E4
 Method BLASTN
 NCBI GI g5902929
 BLAST score 78
 E value 5.0e-36
 Match length 212
 % identity 84
 NCBI Description Oryza sativa mRNA for small GTP-binding protein OsRac3,
 complete cds

Seq. No. 403708
 Seq. ID LIB3433-006-Q6-K6-A4
 Method BLASTX
 NCBI GI g2982251
 BLAST score 169
 E value 1.0e-11
 Match length 101
 % identity 49
 NCBI Description (AF051208) putative RNA-binding protein [Picea mariana]

Seq. No. 403709
 Seq. ID LIB3433-006-Q6-K6-B4
 Method BLASTX
 NCBI GI g5734720
 BLAST score 304
 E value 1.0e-27
 Match length 123
 % identity 50
 NCBI Description (AC008075) Contains PF_01426 BAH (bromo-adjacent homology)
 domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147
 and gb_AA605500 come from this gene. [Arabidopsis thaliana]

Seq. No. 403710
 Seq. ID LIB3433-006-Q6-K6-B6
 Method BLASTX
 NCBI GI g1084461
 BLAST score 384
 E value 6.0e-37
 Match length 133


```
Seq. ID      LIB3433-006-Q6-K6-E1
Method       BLASTX
NCBI GI      g3660467
BLAST score   341
E value      5.0e-32
Match length  89
% identity    76
NCBI Description (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]
```

Seq. No.	403717
Seq. ID	LIB3433-006-Q6-K6-E11
Method	BLASTX
NCBI GI	g2407287
BLAST score	188
E value	4.0e-14
Match length	59
% identity	64
NCBI Description	(AF017366) metallothionein-like protein [Oryza sativa]

```
Seq. No.      403718
Seq. ID       LIB3433-006-Q6-K6-E5
Method        BLASTX
NCBI GI       g21839
BLAST score   469
E value       4.0e-47
Match length  108
% identity    80
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]
```

```
Seq. No.          403719
Seq. ID           LIB3433-006-Q6-K6-E6
Method            BLASTX
NCBI GI           g548770
BLAST score       511
E value           5.0e-52
Match length      121
% identity        83
NCBI Description   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
```

```
Seq. No.      403720
Seq. ID      LIB3433-006-Q6-K6-E7
Method       BLASTX
NCBI GI      g5042453
BLAST score   646
E value      1.0e-67
Match length  126
% identity    97
NCBI Description (AC007789) putative pathogenesis related protein [Oryza sativa]
```

```
Seq. No.      403721
Seq. ID      LIB3433-006-Q6-K6-E9
Method       BLASTN
NCBI GI      q170784
```


Seq. No. 403727
 Seq. ID LIB3433-011-Q6-K1-C4
 Method BLASTX
 NCBI GI g1705735
 BLAST score 403
 E value 3.0e-39
 Match length 79
 % identity 96
 NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11)
 >gi_1362175_pir_S56651 probable calcium-dependent protein
 kinase (clone OSCP11) - rice >gi_587500_emb_CAA57156_
 (X81393) calcium-dependent protein kinase [Oryza sativa]

Seq. No. 403728
 Seq. ID LIB3433-011-Q6-K1-F2
 Method BLASTX
 NCBI GI g4731316
 BLAST score 187
 E value 2.0e-14
 Match length 49
 % identity 76
 NCBI Description (AF120093) elongation factor 1-alpha [Nicotiana tabacum]

Seq. No. 403729
 Seq. ID LIB3433-012-Q6-K1-A11
 Method BLASTN
 NCBI GI g3282393
 BLAST score 313
 E value 1.0e-176
 Match length 395
 % identity 95
 NCBI Description Oryza sativa aie2 mRNA, partial cds

Seq. No. 403730
 Seq. ID LIB3433-012-Q6-K1-B3
 Method BLASTX
 NCBI GI g3914557
 BLAST score 176
 E value 9.0e-13
 Match length 36
 % identity 100
 NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
 PROTEIN) >gi_1155265 (U40219) possible apospory-associated
 protein [Pennisetum ciliare]

Seq. No. 403731
 Seq. ID LIB3433-013-Q6-K1-D11
 Method BLASTN
 NCBI GI g19052
 BLAST score 51
 E value 1.0e-19
 Match length 111
 % identity 87
 NCBI Description H.vulgare Myb1 gene

Seq. No. 403732
 Seq. ID LIB3433-014-Q6-K1-A2

Method BLASTX
 NCBI GI g2865175
 BLAST score 268
 E value 4.0e-36
 Match length 114
 % identity 68
 NCBI Description (AB010945) AtRer1A [Arabidopsis thaliana]
 >gi_4914434_emb_CAB43637.1_ (AL050351) AtRer1A [Arabidopsis thaliana]

Seq. No. 403733
 Seq. ID LIB3433-014-Q6-K1-H12
 Method BLASTX
 NCBI GI g1899025
 BLAST score 186
 E value 5.0e-26
 Match length 91
 % identity 66
 NCBI Description (U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232
 (AC005169) hexokinase [Arabidopsis thaliana]

Seq. No. 403734
 Seq. ID LIB3433-015-Q6-K1-A11
 Method BLASTX
 NCBI GI g388260
 BLAST score 338
 E value 9.0e-32
 Match length 114
 % identity 67
 NCBI Description (X62457) H1-1flk [Arabidopsis thaliana]

Seq. No. 403735
 Seq. ID LIB3433-015-Q6-K1-A9
 Method BLASTN
 NCBI GI g3821780
 BLAST score 36
 E value 8.0e-11
 Match length 36
 % identity 100
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 403736
 Seq. ID LIB3433-015-Q6-K1-B4
 Method BLASTX
 NCBI GI g4512712
 BLAST score 204
 E value 2.0e-16
 Match length 108
 % identity 45
 NCBI Description (AC006569) unknown protein [Arabidopsis thaliana]

Seq. No. 403737
 Seq. ID LIB3433-015-Q6-K1-B6
 Method BLASTX
 NCBI GI g4097342
 BLAST score 450
 E value 1.0e-44

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Match length 84
% identity 49
NCBI Description (U57640) Bowman-Birk type trypsin inhibitor [Oryza sativa]

Seq. No. 403738
Seq. ID LIB3433-015-Q6-K1-B7
Method BLASTX
NCBI GI g4406810
BLAST score 339
E value 6.0e-32
Match length 90
% identity 64
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 403739
Seq. ID LIB3433-015-Q6-K1-B8
Method BLASTX
NCBI GI g2431769
BLAST score 217
E value 1.0e-17
Match length 60
% identity 73
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]

Seq. No. 403740
Seq. ID LIB3433-015-Q6-K1-C10
Method BLASTN
NCBI GI g4097153
BLAST score 63
E value 7.0e-27
Match length 107
% identity 89
NCBI Description Oryza sativa type 1 metallothionein-like (rgMT-1) gene, complete cds

Seq. No. 403741
Seq. ID LIB3433-015-Q6-K1-C3
Method BLASTX
NCBI GI g4850330
BLAST score 321
E value 1.0e-29
Match length 63
% identity 97
NCBI Description (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]

Seq. No. 403742
Seq. ID LIB3433-015-Q6-K1-C6
Method BLASTX
NCBI GI g505136
BLAST score 159
E value 1.0e-12
Match length 54
% identity 76
NCBI Description (D30794) ferredoxin [Oryza sativa]

Seq. No. 403743
Seq. ID LIB3433-015-Q6-K1-D3

09584016-101000

BLAST score 211
E value 9.0e-17
Match length 112
% identity 38
NCBI Description (Z98974) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 403760
Seq. ID LIB3433-017-Q6-K1-H4
Method BLASTN
NCBI GI g6016845
BLAST score 60
E value 5.0e-25
Match length 83
% identity 93
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 403761
Seq. ID LIB3433-017-Q6-K1-H6
Method BLASTX
NCBI GI g121528
BLAST score 292
E value 7.0e-28
Match length 111
% identity 66
NCBI Description GOS9 PROTEIN >gi_100683_pir_S19115 GOS9 protein - rice
>gi_20242_emb_CAA36189_ (X51909) GOS9 [Oryza sativa]

Seq. No. 403762
Seq. ID LIB3433-018-Q6-K6-D4
Method BLASTX
NCBI GI g2429292
BLAST score 197
E value 3.0e-15
Match length 117
% identity 45
NCBI Description (AF014470) peroxidase [Oryza sativa]

Seq. No. 403763
Seq. ID LIB3433-018-Q6-K6-E4
Method BLASTX
NCBI GI g2493147
BLAST score 315
E value 4.0e-29
Match length 77
% identity 84
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574
(U27098) H+-ATPase [Oryza sativa]

Seq. No. 403764
Seq. ID LIB3433-019-P1-K1-A8
Method BLASTX
NCBI GI g1076732
BLAST score 455
E value 2.0e-45
Match length 120
% identity 72
NCBI Description type-1 pathogenesis-related protein - barley

Seq. No.	403774
Seq. ID	LIB3433-020-P1-K1-G2
Method	BLASTX
NCBI GI	g4895197
BLAST score	145
E value	6.0e-09
Match length	44
% identity	59
NCBI Description	(AC007661) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.      403775
Seq. ID       LIB3433-020-P1-K1-G4
Method        BLASTX
NCBI GI       g129591
BLAST score    620
E value       1.0e-64
Match length  135
% identity    93
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
(X16099) phenylalanine ammonia-lyase [Oryza sativa]
```

```
Seq. No.      403776
Seq. ID      LIB3433-020-P1-K1-G6
Method       BLASTX
NCBI GI      g1888357
BLAST score   325
E value      5.0e-34
Match length  148
% identity    55
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
>gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
precursor [Arabidopsis thaliana]
```

```
Seq. No.      403777
Seq. ID      LIB3433-021-P1-K1-C2
Method       BLASTX
NCBI GI      g3335375
BLAST score   521
E value      4.0e-53
Match length  141
% identity    71
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
```

```
Seq. No.      403778
Seq. ID      LIB3433-021-P1-K1-C4
Method       BLASTX
NCBI GI      g4099408
BLAST score   478
E value      4.0e-48
Match length  116
% identity    80
NCBI Description (U86763) delta-type tonoplast intrinsic protein [Triticum aestivum]
```

Seq. No.	403779
Seq. ID	LIB3433-021-P1-K1-G12

Seq. No. 403800
 Seq. ID LIB3433-024-P1-K1-F11
 Method BLASTX
 NCBI GI g398845
 BLAST score 550
 E value 5.0e-61
 Match length 128
 % identity 87
 NCBI Description (X74654) beta3 tubulin [Zea mays]

Seq. No. 403801
 Seq. ID LIB3433-024-P1-K1-G3
 Method BLASTX
 NCBI GI g585551
 BLAST score 499
 E value 1.0e-50
 Match length 112
 % identity 86
 NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
 >gi_629798_pir_S43330 nucleoside-diphosphate kinase (EC
 2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292)
 nucleoside diphosphate kinase [Oryza sativa]

Seq. No. 403802
 Seq. ID LIB3433-024-P1-K1-H1
 Method BLASTX
 NCBI GI g2119055
 BLAST score 222
 E value 2.0e-18
 Match length 57
 % identity 77
 NCBI Description signal recognition particle 54K protein - tomato (cv.
 Rentita)

Seq. No. 403803
 Seq. ID LIB3433-025-P1-K1-G4
 Method BLASTX
 NCBI GI g2529663
 BLAST score 593
 E value 1.0e-61
 Match length 139
 % identity 76
 NCBI Description (AC002535) putative lysophospholipase [Arabidopsis
 thaliana] >gi_3738277 (AC005309) putative lysophospholipase
 [Arabidopsis thaliana]

Seq. No. 403804
 Seq. ID LIB3433-025-P1-K1-G8
 Method BLASTX
 NCBI GI g3298460
 BLAST score 379
 E value 1.0e-36
 Match length 98
 % identity 73
 NCBI Description (AB012268) SAMIPB [Aster tripolium]

000101-91018950

BLAST score 269
E value 9.0e-24
Match length 77
% identity 66
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

Seq. No. 403811
Seq. ID LIB3433-028-P1-K1-E1
Method BLASTN
NCBI GI g287297
BLAST score 41
E value 1.0e-13
Match length 105
% identity 86
NCBI Description Oryza sativa mRNA for aspartate aminotransferase, complete cds

Seq. No. 403812
Seq. ID LIB3433-030-P1-K1-F2
Method BLASTX
NCBI GI g4455206
BLAST score 301
E value 4.0e-27
Match length 181
% identity 44
NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No. 403813
Seq. ID LIB3433-031-P1-K1-A2
Method BLASTX
NCBI GI g100598
BLAST score 485
E value 7.0e-49
Match length 126
% identity 80
NCBI Description ubiquitin / ribosomal protein S27a-1 - barley >gi_167073 (M60175) ubiquitin [Hordeum vulgare]

Seq. No. 403814
Seq. ID LIB3433-031-P1-K1-G8
Method BLASTX
NCBI GI g4006868
BLAST score 350
E value 4.0e-33
Match length 119
% identity 60
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 403815
Seq. ID LIB3433-031-P1-K1-H7
Method BLASTX
NCBI GI g2465151
BLAST score 227
E value 1.0e-18
Match length 115
% identity 46

NCBI Description (Z99753) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 403816
 Seq. ID LIB3433-032-P1-K1-A2
 Method BLASTX
 NCBI GI g5263319
 BLAST score 167
 E value 3.0e-12
 Match length 67
 % identity 49
 NCBI Description (AC007727) ESTs gb_N96028, gb_F14286, gb_T20680, gb_F14443, gb_AA657300 and gb_N65244 come from this gene. [Arabidopsis thaliana]

Seq. No. 403817
 Seq. ID LIB3433-032-P1-K1-E11
 Method BLASTX
 NCBI GI g2462834
 BLAST score 207
 E value 3.0e-16
 Match length 95
 % identity 44
 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403818
 Seq. ID LIB3433-032-P1-K1-G2
 Method BLASTX
 NCBI GI g459895
 BLAST score 292
 E value 1.0e-33
 Match length 86
 % identity 85
 NCBI Description (L29418) sus1 gene product [Zea mays]

Seq. No. 403819
 Seq. ID LIB3433-033-P1-K1-D5
 Method BLASTN
 NCBI GI g1808687
 BLAST score 90
 E value 1.0e-42
 Match length 246
 % identity 89
 NCBI Description S.stapfianus pSD.13 mRNA

Seq. No. 403820
 Seq. ID LIB3433-033-P1-K1-E5
 Method BLASTX
 NCBI GI g1332579
 BLAST score 490
 E value 3.0e-64
 Match length 180
 % identity 8
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 403821
 Seq. ID LIB3433-033-P1-K1-E8
 Method BLASTX

000101-91018960

NCBI GI g1729971
 BLAST score 668
 E value 4.0e-70
 Match length 149
 % identity 87
 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
 (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
 rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
 sativa]

Seq. No. 403822
 Seq. ID LIB3433-033-P1-K1-F10
 Method BLASTX
 NCBI GI g3935141
 BLAST score 342
 E value 6.0e-32
 Match length 109
 % identity 53
 NCBI Description (AC005106) T25N20.5 [Arabidopsis thaliana]

Seq. No. 403823
 Seq. ID LIB3433-033-P1-K1-F4
 Method BLASTX
 NCBI GI g2662310
 BLAST score 521
 E value 7.0e-53
 Match length 106
 % identity 94
 NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 403824
 Seq. ID LIB3433-033-P1-K1-G6
 Method BLASTX
 NCBI GI g283008
 BLAST score 922
 E value 1.0e-100
 Match length 185
 % identity 94
 NCBI Description sucrose synthase (EC 2.4.1.13) - rice
 >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
 sativa]

Seq. No. 403825
 Seq. ID LIB3433-033-P1-K1-H10
 Method BLASTX
 NCBI GI g629858
 BLAST score 580
 E value 8.0e-60
 Match length 129
 % identity 87
 NCBI Description protein kinase C inhibitor - maize

Seq. No. 403826
 Seq. ID LIB3433-034-P1-K1-F7
 Method BLASTX
 NCBI GI g2118425
 BLAST score 243

000001-91048950

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
>gi_1890154_emb_CAA72432_(Y11767) alpha-mannosidase
precursor [Arabidopsis thaliana]

Seq. No. 403832
Seq. ID LIB3433-038-P1-K1-G6
Method BLASTX
NCBI GI g170031
BLAST score 214
E value 3.0e-17
Match length 73
% identity 59
NCBI Description (M10594) nodulin 35 [Glycine max]

Seq. No. 403833
Seq. ID LIB3433-038-P1-K1-G8
Method BLASTX
NCBI GI g2832672
BLAST score 247
E value 5.0e-21
Match length 51
% identity 94
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No. 403834
Seq. ID LIB3433-039-P1-K1-E7
Method BLASTN
NCBI GI g5410347
BLAST score 92
E value 5.0e-44
Match length 383
% identity 87
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No. 403835
Seq. ID LIB3433-040-P1-K1-A7
Method BLASTN
NCBI GI g2331130
BLAST score 62
E value 4.0e-26
Match length 94
% identity 91
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
cds

Seq. No. 403836
Seq. ID LIB3433-040-P1-K1-D7
Method BLASTX
NCBI GI g401138
BLAST score 187
E value 6.0e-14
Match length 105
% identity 46
NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
>gi_418758_pir_S29242 sucrose synthase (EC 2.4.1.13) Ss1 -
barley >gi_19106_emb_CAA46701_(X65871) sucrose synthase
[Hordeum vulgare]

```
Seq. No.          403837
Seq. ID          LIB3433-040-P1-K1-H12
Method          BLASTX
NCBI GI         g462195
BLAST score      437
E value         3.0e-43
Match length     98
% identity       87
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                  >gi_100682_pir_S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
```

```
Seq. No.          403838
Seq. ID          LIB3433-042-P1-K1-D3
Method          BLASTN
NCBI GI         g2773153
BLAST score      158
E value         9.0e-84
Match length     193
% identity       96
NCBI Description  Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
```

```
Seq. No.      403839
Seq. ID      LIB3433-042-P1-K1-H11
Method       BLASTN
NCBI GI      g786129
BLAST score   40
E value      4.0e-13
Match length  48
% identity    96
NCBI Description  Oryza sativa root-specific RCc2 mRNA, complete cds
```

```
Seq. No.          403840
Seq. ID          LIB3433-045-P1-K1-A3
Method          BLASTX
NCBI GI         g2130067
BLAST score      717
E value         5.0e-76
Match length    139
% identity      99
NCBI Description aspartate transaminase (EC 2.6.1.1), mitochondrial - rice
                >gi_2696240_dbj_BAA23815.1_(D67043) aspartate
                aminotransferase [Oryza sativa]
```

```
Seq. No.      403841
Seq. ID      LIB3433-045-P1-K1-B1
Method       BLASTX
NCBI GI      g2117620
BLAST score   177
E value      1.0e-12
Match length  160
% identity    31
NCBI Description peroxidase (EC 1.11.1.7) 1A - alfalfa
```

09684036.101000

>gi_971558_emb_CAA62225_ (X90692) peroxidase1A [Medicago sativa]

Seq. No. 403842
 Seq. ID LIB3433-045-P1-K1-H6
 Method BLASTX
 NCBI GI g1076740
 BLAST score 537
 E value 9.0e-60
 Match length 143
 % identity 78
 NCBI Description chitinase (EC 3.2.1.14) - rice >gi_407472_emb_CAA40107_ (X56787) chitinase [Oryza sativa] >gi_500616_dbj_BAA03750_ (D16222) endochitinase [Oryza sativa]
 >gi_742301_prf__2009354A chitinase [Oryza sativa]

Seq. No. 403843
 Seq. ID LIB3433-048-P1-K1-D4
 Method BLASTN
 NCBI GI g2062705
 BLAST score 32
 E value 4.0e-09
 Match length 32
 % identity 100
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 403844
 Seq. ID LIB3433-048-P1-K1-D6
 Method BLASTX
 NCBI GI g3273243
 BLAST score 377
 E value 1.0e-36
 Match length 78
 % identity 96
 NCBI Description (AB004660) NLS receptor [Oryza sativa]
 >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza sativa]

Seq. No. 403845
 Seq. ID LIB3433-048-P1-K1-E2
 Method BLASTN
 NCBI GI g1196834
 BLAST score 42
 E value 1.0e-14
 Match length 42
 % identity 100
 NCBI Description Oryza sativa (clone 14b) osmotin protein (14b) gene, 3' complete cds

Seq. No. 403846
 Seq. ID LIB3433-048-P1-K1-F6
 Method BLASTN
 NCBI GI g5777612
 BLAST score 97
 E value 4.0e-47
 Match length 228
 % identity 85

NCBI GI g2130073
 BLAST score 406
 E value 1.0e-39
 Match length 131
 % identity 67
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 403853
 Seq. ID LIB3433-052-P1-K1-C4
 Method BLASTX
 NCBI GI g1362010
 BLAST score 155
 E value 2.0e-10
 Match length 47
 % identity 35
 NCBI Description ubiquitin-like protein 9 - Arabidopsis thaliana

Seq. No. 403854
 Seq. ID LIB3433-052-P1-K1-G6
 Method BLASTX
 NCBI GI g4455210
 BLAST score 456
 E value 3.0e-51
 Match length 139
 % identity 73
 NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No. 403855
 Seq. ID LIB3433-053-P1-K1-A7
 Method BLASTN
 NCBI GI g2293567
 BLAST score 78
 E value 7.0e-36
 Match length 92
 % identity 98
 NCBI Description Oryza sativa HvB12D homolog mRNA, complete cds

Seq. No. 403856
 Seq. ID LIB3433-054-P1-K1-D2
 Method BLASTX
 NCBI GI g1173218
 BLAST score 505
 E value 3.0e-51
 Match length 110
 % identity 91
 NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 403857
 Seq. ID LIB3433-055-P1-K1-A3
 Method BLASTX
 NCBI GI g730463

Seq. No. 403867
 Seq. ID LIB3433-056-P1-K1-G3
 Method BLASTX
 NCBI GI g1076732
 BLAST score 328
 E value 1.0e-30
 Match length 85
 % identity 68
 NCBI Description type-1 pathogenesis-related protein - barley
 >gi_732807_emb_CAA88618_ (Z48728) type-1
 pathogenesis-related protein [Hordeum vulgare]

Seq. No. 403868
 Seq. ID LIB3433-057-P1-K1-A2
 Method BLASTX
 NCBI GI g1184112
 BLAST score 216
 E value 5.0e-31
 Match length 97
 % identity 76
 NCBI Description (U46138) Zn-induced protein [Oryza sativa]

Seq. No. 403869
 Seq. ID LIB3433-057-P1-K1-H6
 Method BLASTX
 NCBI GI g3123244
 BLAST score 188
 E value 3.0e-15
 Match length 132
 % identity 41
 NCBI Description ALPHA-MANNOSIDASE IIX (MANNOSYL-OLIGOSACCHARIDE
 1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX)
 >gi_1132479_dbj_BAA09510_ (D55649) alpha mannosidase II
 isozyme [Homo sapiens]

Seq. No. 403870
 Seq. ID LIB3433-058-P1-K1-B9
 Method BLASTN
 NCBI GI g809513
 BLAST score 79
 E value 2.0e-36
 Match length 154
 % identity 88
 NCBI Description Rice mRNA for ferredoxin-nitrite reductase, complete cds

Seq. No. 403871
 Seq. ID LIB3433-058-P1-K1-C1
 Method BLASTX
 NCBI GI g2341025
 BLAST score 221
 E value 7.0e-18
 Match length 63
 % identity 68
 NCBI Description (AC000104) F19P19.2 [Arabidopsis thaliana]

Seq. No. 403872

Seq. ID LIB3433-058-P1-K1-H12
 Method BLASTX
 NCBI GI g1076289
 BLAST score 254
 E value 2.0e-22
 Match length 69
 % identity 57
 NCBI Description amino acid permease AAP5 - Arabidopsis thaliana
 >gi_608673_emb_CAA54632_ (X77501) amino acid permease
 [Arabidopsis thaliana]

Seq. No. 403873
 Seq. ID LIB3433-061-P1-K1-A7
 Method BLASTX
 NCBI GI g4884530
 BLAST score 542
 E value 1.0e-55
 Match length 107
 % identity 98
 NCBI Description (AB027430) beta-1,3-glucanase [Oryza sativa]

Seq. No. 403874
 Seq. ID LIB3433-061-P1-K1-C10
 Method BLASTX
 NCBI GI g3695061
 BLAST score 232
 E value 8.0e-20
 Match length 56
 % identity 80
 NCBI Description (AF064788) rac GTPase activating protein 2 [Lotus japonicus]

Seq. No. 403875
 Seq. ID LIB3433-061-P1-K1-G5
 Method BLASTX
 NCBI GI g21693
 BLAST score 305
 E value 3.0e-28
 Match length 60
 % identity 83
 NCBI Description (X66012) cathepsin B [Triticum aestivum]

Seq. No. 403876
 Seq. ID LIB3433-061-P1-K1-H1
 Method BLASTX
 NCBI GI g2293480
 BLAST score 332
 E value 3.0e-31
 Match length 69
 % identity 91
 NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 403877
 Seq. ID LIB3433-061-P1-K1-H12
 Method BLASTX
 NCBI GI g4388726
 BLAST score 492

% identity	81
NCBI Description	Oryza sativa COX5c mRNA for cytochrome c oxidase subunit 5c, complete cds
Seq. No.	403883
Seq. ID	LIB3434-003-P1-K1-A7
Method	BLASTX
NCBI GI	g3979986
BLAST score	253
E value	3.0e-22
Match length	52
% identity	96
NCBI Description	(Z98866) predicted using Genefinder; similar to Core histone H2A/H2B/H3/H4; cDNA EST EMBL:D71193 comes from this gene; cDNA EST yk477a9.3 comes from this gene; cDNA EST CEESG32RD comes from this gene; cDNA EST yk201g11.3 come
Seq. No.	403884
Seq. ID	LIB3434-003-P1-K1-C2
Method	BLASTX
NCBI GI	g5360230
BLAST score	578
E value	7.0e-60
Match length	106
% identity	99
NCBI Description	(AB015287) Ran [Oryza sativa]
Seq. No.	403885
Seq. ID	LIB3434-004-P1-K1-A2
Method	BLASTX
NCBI GI	g2293480
BLAST score	360
E value	7.0e-36
Match length	85
% identity	95
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]
Seq. No.	403886
Seq. ID	LIB3434-004-P1-K1-B1
Method	BLASTX
NCBI GI	g4567319
BLAST score	735
E value	5.0e-78
Match length	178
% identity	78
NCBI Description	(AC005956) putative copper amine oxidase [Arabidopsis thaliana]
Seq. No.	403887
Seq. ID	LIB3434-004-P1-K1-C4
Method	BLASTN
NCBI GI	g6016845
BLAST score	77
E value	4.0e-35
Match length	93
% identity	96
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

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Seq. No.          403899
Seq. ID           LIB3434-007-P1-K1-G2
Method            BLASTX
NCBI GI           g1729971
BLAST score       235
E value           7.0e-20
Match length      47
% identity        100
NCBI Description   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
                   rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   sativa]
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Seq. No.          403900
Seq. ID           LIB3434-007-P1-K1-H5
Method            BLASTX
NCBI GI           g2662310
BLAST score       391
E value           3.0e-41
Match length      97
% identity        90
NCBI Description   (AB009307) bpwl [Hordeum vulgare]
```

Seq. No.	403901
Seq. ID	LIB3434-008-P1-K1-A1
Method	BLASTN
NCBI GI	g2331130
BLAST score	39
E value	1.0e-12
Match length	75
% identity	89
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

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000101-97048960

Seq. No. 403913
Seq. ID LIB3434-010-P1-K1-H12
Method BLASTX
NCBI GI g3869088
BLAST score 603
E value 8.0e-63
Match length 117
% identity 98
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 403914
Seq. ID LIB3434-011-P1-K1-A2
Method BLASTX
NCBI GI g3859116
BLAST score 337
E value 1.0e-31
Match length 106
% identity 72
NCBI Description (AF031609) unknown [Oryza sativa]

Seq. No. 403915
Seq. ID LIB3434-011-P1-K1-C4
Method BLASTX
NCBI GI g6056413
BLAST score 217
E value 1.0e-17
Match length 55
% identity 82
NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]

Seq. No. 403916
Seq. ID LIB3434-011-P1-K1-G6
Method BLASTN
NCBI GI g5929929
BLAST score 44
E value 1.0e-15
Match length 80
% identity 90
NCBI Description Zea mays voltage-dependent anion channel protein 1b
(vdac1b) mRNA, complete cds; nuclear gene for mitochondrial
product

Seq. No. 403917
Seq. ID LIB3434-012-P1-K1-A3
Method BLASTN
NCBI GI g5922603
BLAST score 201
E value 1.0e-109
Match length 220
% identity 99
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No. 403918
Seq. ID LIB3434-012-P1-K1-E3
Method BLASTN
NCBI GI g2662344

Method	BLASTX
NCBI GI	g5081779
BLAST score	473
E value	1.0e-47
Match length	92
% identity	93
NCBI Description	(AF150630) cellulose synthase [Gossypium hirsutum]
Seq. No.	403930
Seq. ID	LIB3434-015-P1-K1-C1
Method	BLASTN
NCBI GI	g6016845
BLAST score	191
E value	1.0e-103
Match length	251
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.	403931
Seq. ID	LIB3434-015-P1-K1-D1
Method	BLASTX
NCBI GI	g1184774
BLAST score	692
E value	5.0e-73
Match length	157
% identity	85
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	403932
Seq. ID	LIB3434-015-P1-K1-D6
Method	BLASTX
NCBI GI	g4544390
BLAST score	450
E value	1.0e-44
Match length	127
% identity	65
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]
Seq. No.	403933
Seq. ID	LIB3434-015-P1-K1-E1
Method	BLASTX
NCBI GI	g5007084
BLAST score	908
E value	2.0e-98
Match length	172
% identity	98
NCBI Description	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]
Seq. No.	403934
Seq. ID	LIB3434-015-P1-K1-G10
Method	BLASTX
NCBI GI	g2914706
BLAST score	707
E value	9.0e-75
Match length	159


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% identity      72
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.        403940
Seq. ID         LIB3434-016-P1-K1-A11
Method          BLASTN
NCBI GI         g538427
BLAST score     274
E value         1.0e-152
Match length    285
% identity      99
NCBI Description Oryza sativa ribosomal protein S16 mRNA, complete cds

Seq. No.        403941
Seq. ID         LIB3434-016-P1-K1-A2
Method          BLASTX
NCBI GI         g445613
BLAST score     353
E value         2.0e-33
Match length    97
% identity      70
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No.        403942
Seq. ID         LIB3434-016-P1-K1-A7
Method          BLASTN
NCBI GI         g167043
BLAST score     41
E value         1.0e-13
Match length    53
% identity      94
NCBI Description Barley glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
end

Seq. No.        403943
Seq. ID         LIB3434-016-P1-K1-C5
Method          BLASTX
NCBI GI         g1174162
BLAST score     406
E value         1.0e-39
Match length    88
% identity      80
NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis
thaliana] >gi_3746915 (AF091106) E2
ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.        403944
Seq. ID         LIB3434-016-P1-K1-D4
Method          BLASTX
NCBI GI         g1705434
BLAST score     291
E value         3.0e-26
Match length    103
% identity      56
NCBI Description BIBENZYL SYNTHASE >gi_758243_emb_CAA56276_ (X79903)
bibenzyl synthase [Phalaenopsis sp.]

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Seq. No. 403945
 Seq. ID LIB3434-016-P1-K1-E2
 Method BLASTX
 NCBI GI g1710424
 BLAST score 265
 E value 6.0e-28
 Match length 103
 % identity 67
 NCBI Description 50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
 >gi_2129718_pir_S71282 ribosomal protein L21 - Arabidopsis
 thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast
 ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No. 403946
 Seq. ID LIB3434-016-P1-K1-F4
 Method BLASTX
 NCBI GI g2351580
 BLAST score 596
 E value 8.0e-62
 Match length 134
 % identity 82
 NCBI Description (U82433) thymidine diphospho-glucose 4-6-dehydratase
 homolog [Prunus armeniaca]

Seq. No. 403947
 Seq. ID LIB3434-016-P1-K1-H5
 Method BLASTX
 NCBI GI g1519249
 BLAST score 440
 E value 5.0e-44
 Match length 89
 % identity 100
 NCBI Description (U65956) GF14-b protein [Oryza sativa]

Seq. No. 403948
 Seq. ID LIB3434-016-P1-K1-H6
 Method BLASTX
 NCBI GI g133867
 BLAST score 438
 E value 9.0e-48
 Match length 114
 % identity 82
 NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal
 protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
 ribosomal protein S11 [Zea mays]

Seq. No. 403949
 Seq. ID LIB3434-017-P1-K1-A6
 Method BLASTN
 NCBI GI g4835773
 BLAST score 36
 E value 1.0e-10
 Match length 68
 % identity 88
 NCBI Description Arabidopsis thaliana chromosome 1 BAC T16B5 sequence,
 complete sequence

00634016-101000

NCBI GI g1706958
BLAST score 541
E value 2.0e-55
Match length 137
% identity 77
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 403961
Seq. ID LIB3434-025-P1-K1-B9
Method BLASTX
NCBI GI g1477428
BLAST score 199
E value 3.0e-15
Match length 50
% identity 80
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 403962
Seq. ID LIB3434-025-P1-K1-D5
Method BLASTX
NCBI GI g5091616
BLAST score 352
E value 3.0e-33
Match length 179
% identity 44
NCBI Description (AC007454) F23M19.3 [Arabidopsis thaliana]

Seq. No. 403963
Seq. ID LIB3434-025-P1-K1-F2
Method BLASTX
NCBI GI g3290022
BLAST score 373
E value 6.0e-36
Match length 95
% identity 75
NCBI Description (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol) lyase; plastidic isoform [Solanum tuberosum]

Seq. No. 403964
Seq. ID LIB3434-025-P1-K1-H5
Method BLASTX
NCBI GI g5901954
BLAST score 160
E value 1.0e-10
Match length 96
% identity 40
NCBI Description FGFR1 oncogene partner >gi_4454263_emb_CAA77020_ (Y18046)
FGFR1 oncogene partner (FOP) [Homo sapiens]

Seq. No. 403965
Seq. ID LIB3434-026-P1-K1-A2
Method BLASTX
NCBI GI g2583108
BLAST score 343
E value 3.0e-32
Match length 123
% identity 54

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